

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 21, 2004, 08:36:24 ; Search time 21 Seconds
(without alignments)
41.215 Million cell updates/sec

Title: US-09-625-963A-1
Perfect score: 51
Sequence: 1 RMPFNAPYL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.76:**
2: PIR1:**
3: PIR3:**
4: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	410	JC5046	Wilms' tumor suppr
2	51	100.0	448	S33926	Wilms' tumor prote
3	51	100.0	449	A38080	Wilms tumor suscep
4	51	100.0	449	A39692	Wilms' tumor prote
5	41	80.4	213	AD1343	hypothetical prote
6	41	80.4	213	AH1713	hypothetical prote
7	40	78.4	262	G64144	conserved hypochet
8	39	76.5	203	C71375	conserved hypochet
9	38	74.5	205	F83495	probable hydrolase
10	38	74.5	214	AB2195	serine esterase [i
11	38	74.5	581	EB6408	PTH9.11 protein -
12	37	72.5	466	S42210	18G-34k protein -
13	37	72.5	854	S33558	unc-33 protein - C
14	36	70.6	1232	A55478	neuronal apoptosis
15	36	70.6	85	S17463	glutathione transf
16	36	70.6	115	S39393	glutathione transf
17	36	70.6	142	S17462	glutathione transf
18	36	70.6	217	UX0095	glutathione transf
19	36	70.6	218	KURTG4	glutathione transf
20	36	70.6	218	B34159	glutathione transf
21	36	70.6	218	A29036	glutathione transf
22	36	70.6	218	S13202	glutathione transf
23	36	70.6	218	S33860	glutathione transf
24	36	70.6	218	A46143	mu-class glutathio
25	36	70.6	218	A23732	glutathione transf
26	36	70.6	218	A39375	glutathione transf
27	36	70.6	218	S32425	glutathione transf
28	36	70.6	218	A46048	glutathione transf
29	36	70.6	218	S01719	glutathione transf

30	36	70.6	218	2	B28946	glutathione transf
31	36	70.6	218	2	A29794	glutathione transf
32	36	70.6	218	2	A47486	glutathione transf
33	36	70.6	218	2	S65674	glutathione transf
34	36	70.6	220	2	S18464	glutathione transf
35	36	70.6	225	2	A35295	glutathione transf
36	36	70.6	284	2	F95120	hydrolase, probabl
37	36	70.6	284	2	B97990	conserved hypochet
38	36	70.6	358	2	JC5964	apoptosis inhibito
39	36	70.6	381	2	S65212	hypothetical prote
40	36	70.6	382	2	A48492	polyaaccharide exp
41	36	70.6	432	2	B96515	hypothetical prote
42	36	70.6	434	2	C96515	hypothetical prote
43	44	70.6	487	2	T07960	probable (S)-N-met
44	36	70.6	487	2	T07963	probable (S)-N-met
45	36	70.6	618	2	S68450	apoptosis inhibito

ALIGNMENTS

RESULT 1
 JC5046
 Wilms' tumor suppressor protein - African clawed frog
 N:Alternate names: WTI
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 31-Jan-1997
 C/Accession: JC5046
 R:Semba, K.; Salto-Ueno, R.; Takayama, G.; Kondo, M.
 Gene 175, 167-172, 1996
 A>Title: cDNA cloning and its pronephros-specific expression of the Wilms' tumor suppressor protein in the kidney of the African clawed frog.
 A/Reference number: JC5046; PMID:97074667; PMID:8917094
 A/Content: testis
 A:Accession: JC5046
 A:Molecule type: mRNA
 A:Residues: 1-410 <SMB>
 A:Cross-references: DDBJ:DB2051
 C:Comment: This protein is involved in kidney morphogenesis.
 C:Genetics:
 A:Gene: wti

Query Match 100.0%; Score 51; DB 2; Length 410;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMPFNAPYL 9
 Db 107 RMPFNAPYL 115

RESULT 2
 S33926
 Wilms' tumor protein WTI - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 10-May-1996
 C/Accession: S33926
 R:Sharma, P.M.; Yang, X.; Bowman, M.; Roberts, V.; Sukumar, S.
 Cancer Res. 52, 6407-6412, 1992
 A>Title: Molecular cloning of rat Wilms' tumor complementary DNA and a study of messenger RNA expression in rat Wilms' tumor.
 A/Reference number: S33926; PMID:93046155; PMID:1330293
 A:Accession: S33926
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-448 <SHA>
 A:Cross-references: EMBL:X69716
 C:Genetics:
 A:Gene: WTI
 C:Keywords: tumor suppressor

Query Match 100.0%; Score 51; DB 2; Length 448;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 FPNAPYL 9
 |||||
 |||||
 Db 67 FPNAPYL 73

RESULT 6

AH1713
 hypothetical protein homolog lin2252 [imported] - *Listeria innocua* (strain C1p11262)
 C/Species: *Listeria innocua*
 C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C/Accession: AH1713
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fahl, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madeno, E.; Maitournam, A.; Makok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
 A/Reference number: AB1077; MUID:21537279; PMID:11679669
 A/Accession: AH1713
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-213 <GUA>
 A:Cross-references: GB:AL592022; PIDN:CAC97480.1; PID:G16414764; GSPDB:GN00178
 A:Experimental source: strain C1p11262
 C/Genetics:
 A:Gene: lin2252

Query Match 80.4%; Score 41; DB 2; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 FPNAPYL 9
 |||||
 |||||
 Db 67 FPNAPYL 73

RESULT 7

G64144
 hypothetical protein HI0177 - *Haemophilus influenzae* (strain Rd KW20)
 C/Species: *Haemophilus influenzae*
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
 C/Accession: G64144
 R:Reischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Goodyear, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:FPNAPYL: 1-262 <TTGR>
 A:Accession: G64144
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Cross-references: GB:U32703; GB:142023; NID:G1573133; PIDN:AA021847.1; PID:G1573134; T A:Note: best homolog was a hypothetical protein from *Pseudomonas aeruginosa*
 C/Superfamily: conserved hypothetical protein HI0177

Query Match 78.4%; Score 40; DB 1; Length 262;
 Best Local Similarity 75.0%; Pred. No. 3.8;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPNAPY 8
 |||||
 |||||
 Db 151 RVPNAPY 158

RESULT 8

C71375
 conserved hypothetical integral membrane protein TP0033 - *Syphilis spirochete*
 C/Species: *Treponema pallidum* subsp. *pallidum* (syphilis spirochete)
 C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
 C/Accession: C71375

R:Fraser, C.M.; Norris, S.D.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 reon, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Childambaram, M.; Uetzbach, T.; McDor
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A/Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
 A/Reference number: A71250; MUID:98332770; PMID:9665876
 A/Accession: C71375

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-203 <COL>
 A:Cross-references: GB:AE001188; GB:AE000520; NID:G3322282; PIDN:AA065028.1; PID:G3322288
 A:Experimental source: strain Nichols
 C/Genetics:
 A:Gene: TP0033

Query Match 76.5%; Score 39; DB 2; Length 203;
 Best Local Similarity 85.7%; Pred. No. 4.4;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 FPNAPYL 9
 |||||
 |||||
 Db 63 FPNAPYL 69

RESULT 9

F83495
 Probable hydrolase PA1202 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C/Species: *Pseudomonas aeruginosa*
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C/Accession: F83495
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Bro
 adman, S.; Vann, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathog
 A/Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: F83495
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-205 <STO>
 A:Cross-references: GB:AE004550; GB:AE004091; NID:G9947122; PIDN:AA04591.1; GSPDB:GN001:
 A:Experimental source: strain PA01
 C/Genetics:
 A:Gene: PA1202

Query Match 74.5%; Score 38; DB 2; Length 205;
 Best Local Similarity 75.0%; Pred. No. 7;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 MFPNAPYL 9
 |||||
 |||||
 Db 75 MFPQAPYL 82

RESULT 10

AB2195
 serine esterase [imported] - *Nostoc* sp. (strain PCC 7120)
 C/Species: *Nostoc* sp. PCC 7120
 A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C/Accession: AB2195
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurita, T.; Sasamoto, S.; Matsumoto, A.; Iriguchi,
 Nakazaki, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anak*
 A/Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AB2195
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-214 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA074812.1; PID:G17132207; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C/Genetics:

A:Gene: a113113

Query Match 74.5%; Score 38; DB 2; Length 214;
Best Local Similarity 85.7%; Pred. No. 7.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 MFNPAPYL 8
DB 56 VFPNAPY 62

RESULT 11

E86408

F3H9.11 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
A:Accession: E86408
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marzabadi, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86408
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-581 <STO>
A:Cross-references: GB:AE005172; NID:99795613; PIDN:MAP98431.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 74.5%; Score 38; DB 2; Length 581;
Best Local Similarity 87.5%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 8
DB 349 RMPFNAPY 356

RESULT 12

S42210

ISG-54K protein - Chinese hamster
C:Species: Crictetus griseus (Chinese hamster)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 07-May-1999
A:Accession: S42210
R:Bluyssen, H.A.R.; Vlietstra, R.J.; van der Made, A.; Trapman, J.
Eur. J. Biochem. 220, 395-402, 1994
A:Title: The interferon-stimulated gene 54 K promoter contains two adjacent functional alpha inducibility.
A:Reference number: S42210; MUID:94170787; PMID:8125096
A:Accession: S42210
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-466 <BLU>
C:Superfamily: Interferon-induced 56K protein

Query Match 72.5%; Score 37; DB 2; Length 466;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
DB 201 RMSFNAPYV 209

RESULT 13

S33558

unc-33 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 07-Apr-1994 #sequence_revision 02-Jun-1994 #text_change 21-Jul-2000
C:Accession: S33558; S33559; S24643; S24644
R:Li, W.; Herman, R.K.; Shaw, J.E.
Genetics 132, 675-689, 1992

A:Title: Analysis of the Caenorhabditis elegans axonal guidance and outgrowth gene unc-33.
A:Reference number: S33558; MUID:93106371; PMID:1468626
A:Accession: S33558
A:Molecule type: DNA
A:Residues: 1-854 <LIW1>
A:Cross-references: EMBL:214148; NID:96899; PIDN:CAA78520.1; PID:95900
A:Accession: S33559

A:Molecule type: mRNA
A:Residues: 1-854 <LIW2>
A:Cross-references: EMBL:214146; NID:96903; PID:96904
C:Genetics:
A:Insertions: 14/2; 68/1; 129/3; 151/3; 182/1; 255/3; 361/2; 660/1; 790/3
C:Keywords: alternative initiator

F:1-854/Product: unc-33 protein (long form) #status predicted <MAT1>
F:176-854/Product: unc-33 protein (intermediate form) #status predicted <MAT2>
F:332-854/Product: unc-33 protein (short form) #status predicted <MAT3>

Query Match 72.5%; Score 37; DB 2; Length 854;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
DB 773 RLSFNAPYL 781

RESULT 14

A55478

neuronal apoptosis inhibitory protein - human
N:Alternate names: NAIP
C:Species: Homo sapiens (man)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001
A:Accession: A55478
R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shuttler, G.; Yareghi, Z.; Parahani, R.; Baird, S d, T.O.; de Jong, P.J.; Suth, L.; Ikeda, J.B.; Korneluk, R.G.; Mackenzie, A.
Cell 80, 167-178, 1995
A:Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in indiv
A:Reference number: A55478; MUID:95112344; PMID:78133013
A:Accession: A55478
A:Molecule type: mRNA
A:Residues: 1-1232 <ROY>
A:Cross-references: GB:U19251
C:Genetics:
A:Gene: GDB:SMA@; SMA
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A:Map position: Sq12.2-Sq13
C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prote
F:94-110/Domain: transmembrane #status predicted <TM1>
F:470-477/Region: nucleotide-binding motif A (P-loop)
F:479-496/Domain: transmembrane #status predicted <TM2>
F:476/Binding site: ATP (Lys) #status predicted
F:618,632,823,923,1035/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 72.5%; Score 37; DB 2; Length 1232;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
DB 337 RCFNCPFL 345

RESULT 15

S17463

glutathione transferase (EC 2.5.1.18) class mu chain yb5 - mouse (Fragments)
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 16-Feb-1997

C:Accession: S17463
 R:Hayes, J.D.; Kerr, L.A.; Peacock, S.D.; Cronshaw, A.D.; Mclellan, L.I.
 Biochem. J. 277, 501-512, 1991
 A:Title: Hepatic glutathione S-transferases in mice fed on a diet containing the anticarcinogenic elution of the glutathione-Sephadex affinity matrix.
 A:Reference number: S16933; MUID:91315425; PMID:1859377
 A:Accession: S17463

A:Molecule type: protein
 A:Residues: 1-38,39-64,65-85 <RAY>
 C:Superfamily: glutathione transferase
 C:Keywords: blocked amino end; dimer; transferase

Query Match 70.6%; Score 36; DB 2; Length 85;
 Best Local Similarity 85.7%; Pred. No. 6.3;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FPNAPYL 9
 Db 23 FPNLPYL 29

Search completed: January 21, 2004, 08:44:43
 Job time : 22 secs

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OM protein - protein search, using sw model

Run on: January 21, 2004, 08:36:24 ; Search time 11 Seconds
(without alignments)
38.476 Million cell updates/sec

Title: US-09-625-963A-1
Perfect score: 51
Sequence: 1 RMPFNAPYL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	448	1	WT1_RAT
2	51	100.0	449	1	WT1_HUMAN
3	51	100.0	449	1	WT1_MOUSE
4	51	100.0	449	1	WT1_PIG
5	40	78.4	262	1	YPTO_HAERL
6	37	72.5	468	1	IFP2_CRILLO
7	37	72.5	854	1	UNO3_CAEEL
8	37	72.5	1403	1	BIR1_HUMAN
9	36	70.6	217	1	GTMI_HUMAN
10	36	70.6	217	1	GTMI_MOUSE
11	36	70.6	217	1	GTMI_RAT
12	36	70.6	217	1	GTMI_HUMAN
13	36	70.6	217	1	GTM2_MOUSE
14	36	70.6	217	1	GTM2_RAT
15	36	70.6	217	1	GTM3_MOUSE
16	36	70.6	217	1	GTM3_RAT
17	36	70.6	217	1	GTM5_HUMAN
18	36	70.6	217	1	GTMU_CAVO
19	36	70.6	217	1	GTMU_CRILLO
20	36	70.6	217	1	GTMU_MESAU
21	36	70.6	217	1	GTMU_RABRT
22	36	70.6	218	1	GTM4_HUMAN
23	36	70.6	218	1	GTM6_MOUSE
24	36	70.6	219	1	GTM6_CHICK
25	36	70.6	224	1	GTM3_HUMAN
26	36	70.6	224	1	GTM5_MOUSE
27	36	70.6	226	1	BSH_DROME
28	36	70.6	358	1	PIAF_PIG
29	36	70.6	370	1	TPSI_HUMAN
30	36	70.6	370	1	TPSI_MOUSE
31	36	70.6	381	1	R8AI_YEAST
32	36	70.6	382	1	KSEI_ECOLI
33	36	70.6	382	1	KSB5_ECOLI

RESULT 1	ID	WT1_RAT	STANDARD	PRT	448 AA.
34	36	70.6	487	1	CSB1_ESCCA
35	36	70.6	488	1	CSB2_ESCCA
36	36	70.6	509	1	CAA1_DROME
37	36	70.6	618	1	BIR2_HUMAN
38	35	68.6	273	1	TRY6_ANOGA
39	35	68.6	380	1	TPSA_CAEEL
40	35	68.6	500	1	C81F_ARATH
41	34	66.7	180	1	YH95_AOUAE
42	34	66.7	260	1	YH20_PASMU
43	34	66.7	855	1	ST14_MOUSE
44	34	66.7	1097	1	CCT_DROME
45	33	64.7	110	1	YA61_STRMU

ALIGNMENTS

WT1_RAT
P49952;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
DE Wilms' tumor protein homolog.
WT1 OR WT-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
[1]
SEQUENCE FROM N.A. (ISOPFORMS 1; 2; 3 AND 4).
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=93046155; Pubmed=1330293;
RA Sharma P.M., Yang X., Bowman M., Roberts V., Sukumar S.;
RT "Molecular cloning of rat Wilms' tumor complementary DNA and a study
of messenger RNA expression in the urogenital system and the brain.";
Rl Cancer Res. 52:6407-6412(1992).
CC -1- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES
AND BINDS TO THE DNA SEQUENCE 5'-CGCCCCGC-3'.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=P49952-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P49952-2; Sequence=VSP_006872, VSP_006873;
CC Name=3;
CC IsoId=P49952-3; Sequence=VSP_006872;
CC Name=4;
CC IsoId=P49952-4; Sequence=VSP_006873;
CC -1- TISSUE SPECIFICITY: Kidney.
CC -1- DEVELOPMENTAL STAGE: Expressed during kidney development.
CC -1- SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER
PROTEINS.
CC -1- SIMILARITY: Contains 4 C2H2-type zinc fingers.

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or send an email to license@1sb-sib.ch).

CC EMBL: X69716; CAA49373.1; --
CC HSSP: P08046; 1AAY.
CC TRANSFAC: T02352;
DR InterPro: IPR000976; Wilms tumour.
DR InterPro: IPR007087; znf_C2H2.
DR Pfam: PF02165; WT1; 1.
DR Pfam: PF00096; zf-C2H2; 4.
DR PRINTS: PR00049; WILMSTUMOUR.

RL Cell 67:437-447(1991).
 RN [13]
 RP VARIANTS DDS
 RX MEDLINE=93266053; PubMed=1338906;
 RA Baird P.N., Santos A., Groves N., Jadresic L., Cowell J.K.;
 RT "Constitutional mutations in the WT1 gene in patients with
 RT Denys-Drash syndrome.";
 RL Hum. Mol. Genet. 1:301-305(1992).
 RN [14]
 RP SEQUENCE OF 385-405 FROM N.A., AND VARIANT DDS TRP-394.
 RX MEDLINE=93250986; PubMed=1302008;
 RA Brenning W., Hausen N., Silberman B.L., Cohn R.A., Machin G.A.,
 RA Aronson A.J., Housman D., Pelletier J.;
 RT "Germline intronic and exonic mutations in the Wilms' tumour gene
 RT (WT1) affecting urogenital development.";
 RL Nat. Genet. 1:144-148(1992).
 RN [15]
 RP VARIANTS DDS.
 RX MEDLINE=93271983; PubMed=8388765;
 RA Little M.H., Williamson K.A., Mannens M., Kelsey A., Gosden C.,
 RA Haseltine N.D., van Heyningen V.;
 RT "Evidence that WT1 mutations in Denys-Drash syndrome patients may act
 RT in a dominant-negative fashion.";
 RL Hum. Mol. Genet. 2:259-264(1993).
 RN [16]
 RP VARIANTS DDS TRP-394 AND PRO-398.
 RX MEDLINE=94125627; PubMed=8295405;
 RA Takeda M., Sakiyama T., Kitagawa T., Watanabe S., Watanabe T.,
 RA Takahashi S., Kawaguchi H., Ito K.;
 RT "Molecular analysis of two Japanese cases of Denys-Drash syndrome.";
 RL J. Inher. Metab. Dis. 16:876-880(1993).
 RN [17]
 RP VARIANT MESOTHELIOMA GLY-273.
 RX MEDLINE=94004972; PubMed=8401592;
 RA Park S., Schalling M., Bernard A., Maheswaran S., Shipley G.C.,
 RA Roberts J., Fletcher J., Shipman R., Rheinwald J., Demetri G.,
 RA Griffin J., Minden M., Housman D.E., Haber D.A.;
 RT "The Wilms tumour gene WT1 is expressed in murine mesoderm-derived
 RT tissues and mutated in a human mesothelioma.";
 RL Nat. Genet. 4:415-420(1993).
 RN [18]
 RP VARIANT DDS ARG-377.
 RX MEDLINE=94156335; PubMed=8112732;
 RA Nordenskjold A., Friedman E., Anyret M.;
 RT "WT1 mutations in patients with Denys-Drash syndrome: a novel mutation
 RT in exon 8 and paternal allele origin.";
 RL Hum. Genet. 93:115-120(1994).
 RN [19]
 RP VARIANT DDS TYR-373.
 RX MEDLINE=97114281; PubMed=8956030;
 RA Gahremani M., Chan C.B., Bistritz T., Aladjem M.M., Tieder M.,
 RA Pelletier J.;
 RT "A novel mutation H373 in the Wilms' tumor suppressor gene, WT1,
 RT associated with Denys-Drash syndrome.";
 RL Hum. Hered. 46:336-338(1996).
 RN [20]
 RP VARIANTS WT SER-181 AND ATA-253.
 RX MEDLINE=97266681; PubMed=9108089;
 RA Schumacher V., Schneider S., Figue A., Wildhardt G., Harms D.,
 RA Schmidt D., Weirich A., Ludwig R., Royer-Pokora B.;
 RT "Correlation of germ-line mutations and two-hit inactivation of the
 RT WT1 gene with Wilms tumors of stromal-predominant histology.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3972-3977(1997).
 RN [21]
 RP VARIANTS IDMS TYR-377; LEU-383 AND ASN-396, VARIANTS DDS CVS-366;
 RP GUN-394; TRP-394 AND PRO-398, AND VARIANT WT ASN-223.
 RX MEDLINE=98198341; PubMed=9529364;
 RA Jeunpierre C., Denamur E., Henry I., Cabanis M.-O., Luce S.,
 RA Cecille A., Blon J., Peuchmann M., Lotrat C., Naudat P.,
 RA Gubler M.-C., Junien C.;
 RT "Identification of constitutional WT1 mutations, in patients with
 RT isolated diffuse mesangial sclerosis, and analysis of
 RT genotype/phenotype correlations by use of a computerized mutation

RT database.";
 RL Am. J. Hum. Genet. 62:824-833(1998).
 RN [22]
 RP VARIANTS DDS TYR-355, HIS-366 AND ARG-385.
 RX MEDLINE=9815435; PubMed=9475094;
 RA Kikuchi H., Takata A., Akasaka Y., Fukuzawa R., Yoneyama H.,
 RA Kurosawa Y., Honda M., Kamiyama Y., Hata J.;
 RT "Do intronic mutations affecting splicing of WT1 exon 9 cause Fraiser
 RT syndrome?"
 Query Match 100.0%; Score 51; DB 1; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RMPFNAPYL 9
 Db 126 RMPFNAPYL 134
 RESULT 3
 WT1_MOUSE STANDARD; PRT; 449 AA.
 AC P22561;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Wilms' tumor protein homolog.
 GN WT1 OR WT-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
 RX MEDLINE=91141522; PubMed=1671709;
 RA Buckler A.J., Pelletier J., Haber D.A., Glaser T., Housman D.E.;
 RT "Isolation, characterization, and expression of the murine Wilms'
 RT tumor gene (WT1) during kidney development.";
 RL Mol. Cell. Biol. 11:1707-1712(1991).
 CC -1- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES
 CC AND BINDS TO THE DNA SEQUENCE 5'-CGCCCCGC-3'.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Evnt=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC Name=2;
 CC Name=3;
 CC Name=4;
 CC IsoId=P22561-2; Sequence=VSP_006868, VSP_006869;
 CC IsoId=P22561-3; Sequence=VSP_006868;
 CC Name=4;
 CC IsoId=P22561-4; Sequence=VSP_006869;
 CC -1- TISSUE SPECIFICITY: Kidney.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING KIDNEY DEVELOPMENT.
 CC -1- SIMILARITY: BELONGS TO THE BGR FAMILY OF C2H2-TYPE ZINC-FINGER
 CC PROTEINS.
 CC -1- SIMILARITY: Contains 4 C2H2-type zinc fingers.
 CC -----
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 CC -----
 CC EMBL; M55512; AAA40573.1; -.
 DR HSSP; P08046; 1AA1; -.
 DR TRASNFPAC; T02351; -.
 DR MGD; MGI:98968; W1.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0005515; F:protein binding activity; IPI.
 DR GO; GO:0001654; P:eye morphogenesis; IMP.

DR GO:0006357, P:regulation of transcription from Pol II pro. . . ; IDA.
 DR InterPro: IPR000976; Wilms tumour.
 DR Pfam: PF02165; WT1, 1.
 DR Pfam: PF00096; Zf-C2H2, 4.
 DR PRINTS: PR00049; WILMSTUMOUR.
 DR PRODOM: PD000003; Znf_C2H2, 2.
 DR SMART: SM00355; Znf_C2H2, 4.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 4.
 DR Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
 KW Transcription regulation; Alternative splicing; Anti-oncogene.
 FT DOMAIN 28 83 PRO-RICH.
 FT ZN_FING 323 347 C2H2-TYPE 1.
 FT ZN_FING 353 377 C2H2-TYPE 2.
 FT ZN_FING 383 405 C2H2-TYPE 3.
 FT ZN_FING 414 438 C2H2-TYPE 4.
 FT VARSPLIC 250 266 Missing (in isoform 2 and isoform 3).
 FT VARSPLIC 408 410 /FTId=VSP_006868.
 FT VARSPLIC Missing (in isoform 2 and isoform 4).
 FT VARSPLIC /FTId=VSP_006869.
 SQ SEQUENCE 449 AA; 49246 MW; 96238189C8D7A380 CRC64;
 Query Match 100.0%; Score 51; DB 1; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RMPFNAPYL 9
 Db 126 RMPFNAPYL 134
 RESULT 4
 ID_WT1_PIG STANDARD; PRT; 449 AA.
 AC O62651;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Wilms' tumor protein homolog.
 GN WT1.
 OS Sus scrofa (Pig).
 CC Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_Taxid=9823;
 RP [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
 RC STRAIN=LMD; TISSUE=Kidney;
 FX MEDLINE=98267201; Pubmed=9602131;
 RA Tsurutani N., Oda H., Nakatsuru Y., Imai Y., Zhang S., Ueno Y.,
 RA Ishikawa T.;
 RT "cDNA cloning and developmental expression of the porcine homologue
 of WT1.";
 RL Gene 211;215-220(1998).
 CC -1- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES
 AND BINDS TO THE DNA SEQUENCE 5'-CGCCCGC-3'.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Experimental confirmation may be lacking for some
 isoforms;
 CC Name=1;
 CC IsoId=O62651-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O62651-2; Sequence=VSP_006870, VSP_006871;
 CC Name=3;
 CC IsoId=O62651-3; Sequence=VSP_006870;
 CC Name=4;
 CC IsoId=O62651-4; Sequence=VSP_006871;
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING KIDNEY DEVELOPMENT.
 CC -1- SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER
 PROTEINS.
 CC -1- SIMILARITY: Contains 4 C2H2-type zinc fingers.

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 or send an email to license@1sb-sib.ch).

 CC EMBL; AB010969; BAA28147.1; -.
 DR HSSP; P08046; 1AA1.
 DR InterPro: IPR000976; Wilms tumour.
 DR InterPro: IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WT1, 1.
 DR Pfam; PF00096; Zf-C2H2, 4.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR PRODOM; PD000003; Znf_C2H2, 2.
 DR SMART; SM00355; Znf_C2H2, 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 DR Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
 KW Transcription regulation; Alternative splicing; Anti-oncogene.
 FT DOMAIN 28 83 PRO-RICH.
 FT ZN_FING 323 347 C2H2-TYPE 1.
 FT ZN_FING 353 377 C2H2-TYPE 2.
 FT ZN_FING 383 405 C2H2-TYPE 3.
 FT ZN_FING 414 438 C2H2-TYPE 4.
 FT VARSPLIC 249 265 Missing (in isoform 2 and isoform 3).
 FT VARSPLIC /FTId=VSP_006870.
 FT VARSPLIC Missing (in isoform 2 and isoform 4).
 FT VARSPLIC /FTId=VSP_006871.
 SQ SEQUENCE 449 AA; 49166 MW; 9C35575965A7B3 CRC64;
 Query Match 100.0%; Score 51; DB 1; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RMPFNAPYL 9
 Db 126 RMPFNAPYL 134
 RESULT 5
 YFTO_HAEMIN STANDARD; PRT; 262 AA.
 ID_YFTO_HAEMIN
 AC P44553;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Putative lipoprotein H10177 precursor.
 GN H10177.
 OS Haemophilus influenzae.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 CC Pasteurellales; Haemophilus.
 OX NCBI_Taxid=727;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 FX MEDLINE=95350630; Pubmed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shilly R., Liu L.-I., Glodok A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrman J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 Rd.";
 RL Science 269:496-512(1995).
 RN [2]
 RN IDENTIFICATION BY MASS SPECTROMETRY.

CC EMBL; Z14148; CAA78520.1; -
 DR EMBL; Z14148; CAA78521.1; -
 DR EMBL; Z14148; CAA78522.1; -
 DR EMBL; Z14146; CAA78516.1; -
 DR EMBL; Z14146; CAA78517.1; -
 DR EMBL; Z14146; CAA78518.1; -
 DR EMBL; AC006737; AAM97966.1; -
 DR EMBL; AC006737; AAM97966.1; -
 DR PIR; S33558; S33558. -
 DR Wormpep; Y37E11C.1a; CE31557.
 DR Wormpep; Y37E11C.1b; CE31638.
 DR Wormpep; Y37E11C.1c; CE31639.
 DR InterPro; IPR006680; Amdohydro_1.
 DR InterPro; IPR005847; Urease.
 DR Pfam; PF01979; Amdohydro_1; 1.
 DR Pfam; PD000518; Urease; 1.
 DR Aternative splicing.
 KM VASPLIC 1 175 Missing (in isoform II).
 FT VASPLIC 1 331 /FTId=VSP_001310.
 FT VASPLIC 1 331 Missing (in isoform III).
 FT VASPLIC 1 331 /FTId=VSP_001311.
 SQ SEQUENCE 854 AA; 90819 MW; A8073DD5251D2D77 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 854;
 Best Local Similarity 66.7%; Pred. No. 26;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Gy 1 RMPNAPYL 9
 Db 773 RLSNSPFL 781

RESULT 8
 BIR1_HUMAN STANDARD; PRT; 1403 AA.
 AC Q13075; Q75857; Q13730; Q99796;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis
 DE inhibitory protein).
 GN BIR1 OR NAIP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=95112344; PubMed=7813013;
 RA Roy N., Mahadevan M.S., McLean M., Shuttler G., Yavraghi Z.,
 RA Farahani R., Baird S., Besner-Johnston A., Lefebvre C., Zhang X.,
 RA Saitoh M., Aubry H., Tamai K., Guan X., Ioannou P., Crawford T.O.,
 RA de Jong P.J., Suth L., Ikeda J., Korneluk R.G., Mackenzie A.;
 RA "The gene for neuronal apoptosis inhibitory protein is partially
 RA deleted in individuals with spinal muscular atrophy.";
 RL Cell 80:167-178(1995).
 RN [2]
 RP SEQUENCE FROM N.A. AND REVISIONS.
 RC TISSUE=Brain;
 RX MEDLINE=9616755; PubMed=9503025;
 RA Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farahani R.,
 RA Xuan J.-Y., Kang X., Lefebvre C., Ikeda J.-E., Korneluk R.G.,
 RA Mackenzie A.E.;
 RA "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular
 RA atrophy candidate genes SMN and NAIP.";
 RL Genomics 48:121-127(1998).
 RN [3]
 RP SEQUENCE OF 386-623 FROM N.A.
 RA der Steege G., Draalijers T.G., Grootsoorten P.M., Ozinga J.,
 RA Mammano R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,

RA Buys C.H.C.M.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 222-1403 FROM N.A.
 RA Jones K., Graves T., McPherson J.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP FUNCTION.
 RC TISSUE=Liver;
 RX MEDLINE=96149249; PubMed=8552191;
 RA Libton P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
 RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
 RA "Suppression of apoptosis in mammalian cells by NAIP and a related
 RA family of IAP genes.";
 RL Nature 379:349-353(1996).
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
 CC SIGNALS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY
 CC NEURONS. FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN
 CC SPINAL CORD.
 CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN
 CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE 1). SMAS
 CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE I
 CC (WERDNIG-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE
 CC III (WOLFFHART-KUGELBERG-WELANDER DISEASE) BASED UPON THE AGE OF
 CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE
 CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO
 CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000
 CC NEWBORNS.
 CC -1- SIMILARITY: Contains 3 BIR repeats.
 CC -1- SIMILARITY: Contains 1 NACHT domain.
 CC -----
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 CC -----
 CC EMBL; U19251; AAC52045.1; -
 CC EMBL; U80017; AAC52047.1; -
 CC EMBL; U21913; AAA64504.1; -
 CC EMBL; AC005031; AAC62261.1; -
 CC HSSP; Q13490; IQSH.
 CC GeneW; HGNC:7634; BIR1.
 CC MIM; 600355; -
 CC GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
 CC GO; GO:0006916; P:anti-apoptosis; TAS.
 CC GO; GO:0007399; P:neurogenesis; TAS.
 CC InterPro; IPR003593; AAA_Alpase.
 CC InterPro; IPR01370; BIR.
 CC InterPro; IPR007111; NACHT_NTPase.
 CC Pfam; PF00653; BIR; 3.
 CC SMART; SM00238; AAA; 1.
 CC PROSITE; PS01282; BIR_REPEAT_1; 3.
 CC PROSITE; PS50143; BIR_REPEAT_2; 3.
 CC PROSITE; PS50837; NACHT; 1.
 KW Apoptosis; Repeat.
 FT REPEAT 60 127 BIR 1.
 FT REPEAT 159 227 BIR 2.
 FT REPEAT 278 345 BIR 3.
 FT DOMAIN 464 758 NACHT.
 FT CONFLICT 222 223 PK -> YR (IN REF. 4).
 FT CONFLICT 386 387 VP -> ST (IN REF. 3).
 FT CONFLICT 535 535 M -> V (IN REF. 3).
 FT CONFLICT 553 553 Y -> H (IN REF. 3).
 FT CONFLICT 1228 1231 MISSING (IN REF. 4).
 FT SEQUENCE 1403 AA; 159613 MW; 566304C154D5E64 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 1403;
 Best Local Similarity 66.7%; Pred. No. 45;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RMPNAPYL 9
 DB 337 RCFPCPPL 345

RESULT 9
 GTM1_HUMAN STANDARD; PRT; 217 AA.
 ID GTM1_HUMAN
 AC P09489;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glutathione S-transferase Mu 1 (EC 2.5.1.18) (GSTM1-1) (HB subunit 4)
 DE (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1).
 GN GSTM1 OR GST1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBT_TaxID=9606;
 RN NM
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88335606; PubMed=3419925;
 RA DeJong J.L., Chang C.M., Whang Peng J., Knutsen T., Tu C.-P.D.;
 RT "The human liver glutathione S-transferase gene superfamily:
 RL expression and chromosome mapping of an Hb subunit cDNA.";
 RL Nucleic Acids Res. 16:8541-8554(1988).
 RN NM
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89017184; PubMed=3174634;
 RA Seidegaard J., Vorachek W.R., Pero R.W., Pearson W.R.;
 RT "Hereditary differences in the expression of the human glutathione
 RL transferase active on trans-stilbene oxide are due to a gene
 RT deletion.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7293-7297(1988).
 RN NM
 RP SEQUENCE OF 1-188 FROM N.A.
 RX MEDLINE=93228631; PubMed=8471052;
 RA Zhong S., Spurr N.K., Hayes J.D., Wolf C.R.;
 RT "Deduced amino acid sequence, gene structure and chromosomal location
 RL of a novel human class Mu glutathione S-transferase, GSTM4.";
 RL Biochem. J. 291:41-50(1993).
 RN NM
 RP SEQUENCE OF 59-117 FROM N.A.
 RX MEDLINE=90301515; PubMed=2362832;
 RA Comstock K.E., Sanderson B.J.S., Clafilin G., Henaar W.D.;
 RT "GST1 gene deletion determined by polymerase chain reaction.";
 RL Nucleic Acids Res. 18:3670-3670(1990).
 RN NM
 RP SEQUENCE OF 1-23.
 RX MEDLINE=86042634; PubMed=3864155;
 RA Mannervik B., Alin P., Guthenberg C., Jansson H., Tahir M.K.,
 RA Warholm M., Joernvall H.;
 RT "Identification of three classes of cytosolic glutathione transferase
 RL data and enzymatic properties.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7202-7206(1985).
 RN NM
 RP SEQUENCE OF 1-23.
 RX MEDLINE=85154554; PubMed=3979555;
 RA Alin P., Mannervik B., Joernvall H.;
 RT "Structural evidence for three different types of glutathione
 RL transferase in human tissues.";
 RL FEBS Lett. 182:319-322(1985).
 RN NM
 RP SEQUENCE OF 52-59, AND MASS SPECTROMETRY.
 RX MEDLINE=21088920; PubMed=11271497;
 RA Hubbard M.J., Mchugh N.J.;
 RT "Human ERp29: Isolation, primary structural characterisation and two-
 RL dimensional gel mapping.";
 RL Electrophoresis 21:3785-3796(2000).

[8]
 RP X-RAY CRYSTALLOGRAPHY (2.68 ANGSTROMS), AND MUTAGENESIS OF HIS-107.
 RX MEDLINE=99130249; PubMed=9930979.
 RA Patzkovsky Y.V., Patzkovska L.N., Listovsky I.;
 RT "Functions of His107 in the catalytic mechanism of human glutathione
 RL S-transferase hGSTM1a-1a.";
 RL Biochemistry 38:1193-1202(1999).
 CC -1- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER
 CC OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
 CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: THIS IS A LIVER ISOZYME.
 CC -1- POLYMORPHISM: THERE ARE TWO ALLELES, GSTM1A AND GSTM1B WHICH
 CC DIFFER IN POSITION 172.
 CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. NO FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X08020; CAA30821.1; -;
 CC EMBL; J03817; ABA52203.1; -;
 CC EMBL; X68676; CAA48636.1; -;
 CC EMBL; X51451; CAA35817.1; -;
 CC PIR; S01719; S01719.
 CC PDB; 1GTU; 02-FEB-99.
 CC GeneW; HGNC:4632; GSTM1.
 DR MIR; 138350; -;
 DR GO; GO:0004364; P:glutathione transferase activity; TAS.
 DR GO; GO:0008181; F:tumor suppressor; TAS.
 DR InterPro; IPR004046; GST_Cterm.
 DR InterPro; IPR003081; GST_mu.
 DR InterPro; IPR004045; GST_Nterm.
 DR Pfam; PF00043; GST_C; 1.
 DR Pfam; PF02798; GST_N; 1.
 DR PRINTS; PRO1267; GSTRNSFRASEM.
 DR TRANSFERASE; Multigene family; Polymorphism; 3D-structure.
 KW INT MET 0
 FT VARIANT 172 172
 FT VARIANT 209 209
 FT VARIANT 107 107
 FT MUTAGEN 107 107
 FT CONFLICT 43 43
 FT STRAND 2 7
 FT HELIX 11 13
 FT HELIX 14 22
 FT TURN 23 24
 FT TURN 22 22
 FT STRAND 27 32
 FT HELIX 43 49
 FT TURN 50 50
 FT STRAND 61 64
 FT STRAND 65 66
 FT TURN 67 70
 FT STRAND 72 82
 FT HELIX 83 84
 FT HELIX 90 115
 FT TURN 117 118
 FT HELIX 119 141
 FT TURN 142 143
 FT STRAND 144 146
 FT STRAND 147 148
 FT STRAND 149 149
 FT HELIX 154 169
 FT TURN 171 176
 FT HELIX 178 188
 FT TURN 189 189
 K -> N (IN ALLELE GSTM1B).
 /FTID=VAR_003617.
 S -> T (IN DBSNP:449856).
 /FTID=VAR_014497.
 H -> S: CHANGE THE PROPERTIES OF THE ENZYME
 TOWARD SOME SUBSTRATES.
 S -> T (IN REF. 3).

FT HELIX 191 197
 FT TURN 198 198
 FT TURN 210 211
 SQ SEQUENCE 217 AA; 25580 MW; ABBB08713BA75EAB CRC64;
 Query Match Similarity 70.6%; Score 36; DB 1; Length 217;
 Best Local Similarity 85.7%; Pred. No. 9.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPNAPYL 9
 56 PPNAPYL 62

RESULT 10
 GTM1 MOUSE STANDARD; PRT; 217 AA.
 AC P10649;
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glutathione S-transferase Mu 1 (EC 2.5.1.18) (GST class-mu 1)
 DE (Glutathione S-transferase GST-7) (pmGT10) (GST 1-1).
 GN GSTM1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89330838; PubMed=3417659;
 RA Pearson W.R.; Reinhart J.; Sisk S.C.; Anderson K.S.; Adler P.N.;
 RA "Tissue-specific induction of murine glutathione transferase mRNAs by
 RA butyrlated hydroxyanisole.";
 RA J. Biol. Chem. 263:13324-13332(1988).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=900943277; PubMed=2689439;
 RA Townsend A.J.; Goldsmith M.E.; Pickett C.B.; Cowan K.H.;
 RA "Isolation, characterization, and expression in Escherichia coli of
 RA two murine Mu class glutathione S-transferase cDNAs homologous to the
 RA rat subunits 3 (Yb1) and 4 (Yb2).";
 RA J. Biol. Chem. 264:21582-21590(1989).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93290350; PubMed=8512223;
 RA Reinhart J.; Pearson W.R.;
 RA "The structure of two murine class-mu glutathione transferase genes
 RA coordinately induced by butyrlated hydroxyanisole.";
 RA Arch. Biochem. Biophys. 303:383-393(1993).
 RL [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22388257; PubMed=12477932;
 RA Straubeberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shemen C.M.; Schuler G.D.;
 RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Hsieh M.K.;
 RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
 RA Datchenko L.; Martina K.; Farmer A.A.; Rubin G.M.; Hong L.;
 RA Stadelson M.; Soares M.B.; Bonaldi M.F.; Casavant T.L.; Scheetz T.E.;
 RA Brownstein M.J.; Ustin T.B.; Toshiyuki S.; Carrinzi P.; Prange C.;
 RA Raha S.S.; Loguelfano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
 RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
 RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hallik S.W.;
 RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
 RA Fahy J.; Hellon E.; Kettelman M.; Madan A.C.; Rodrigues S.; Sanchez A.;
 RA Whiting M.; Madan A.C.; Shevchenko Y.; Bouffard G.G.;
 RA Bikesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
 RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;
 RA Roderfeldt Y.S.N.; Krzywinski M.I.; Skalska U.; Smalins D.E.;
 RA Scherter A.; Schein J.E.; Jones S.J.M.; Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 RA human and mouse cDNA sequences.";
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [5]
 RP PRELIMINARY SEQUENCE OF 1-40.
 RX MEDLINE=83109018; PubMed=6822548;
 RA Pearson W.R.; Windle U.J.; Morrow J.F.; Benson A.M.; Talalay P.;
 RA "Increased synthesis of glutathione S-transferases in response to
 RA anticarcinogenic antioxidants. Cloning and measurement of messenger
 RA RNA.";
 RL J. Biol. Chem. 258:2052-2062(1983).
 RN [6]
 RP PRELIMINARY SEQUENCE OF 1-24.
 RX MEDLINE=86042634; PubMed=3864155;
 RA Mannervik B.; Alin P.; Guttenberg C.; Jansson H.; Tahir M.K.;
 RA Warholm M.; Joernvall H.;
 RA "Identification of three classes of cytosolic glutathione transferase
 RA common to several mammalian species: correlation between structural
 RA data and enzymatic properties.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7202-7206(1985).
 RN [7]
 RP CHARACTERIZATION.
 RC STRAIN=CD-1; TISSUE=Liver;
 RX MEDLINE=96189427; PubMed=8605288;
 RA Mitchell A.E.; Morin D.; Lame M.W.; Jones A.D.;
 RA "Purification, mass spectrometric characterization, and covalent
 RA modification of murine glutathione S-transferases.";
 RL Chem. Res. Toxicol. 8:1054-1062(1995).
 CC -1- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER
 CC OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
 CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MASS SPECTROMETRY: MW=25838.4; MW_ERR=2; METHOD=Electrospray.
 CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY.
 CC -----
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 CC -----
 DR EMBL: J03952; AAA37747.1; --
 DR EMBL: J04632; AAA37705.1; --
 DR EMBL: I13448; -- NOT ANNOTATED_CDS.
 DR EMBL: BC003822; AAR03822.1; --
 DR PIR: S33860; S33860.
 DR HSSP: P04905; 2GST.
 DR SWISS-2DPAGE: P10649; MOUSE.
 DR MGD: MGI:95860; Gstm1.
 DR InterPro: IPR004046; GST_Cterm.
 DR InterPro: IPR003081; GST_mu.
 DR InterPro: IPR004045; GST_Nterm.
 DR Pfam: PF00043; GST_C; 1.
 DR Pfam: PF02798; GST_N; 1.
 DR PRINTS: PR01267; GSTPNSFRASEM.
 KM Transferase; Multigene family.
 FT INT MET 0
 FT SEQUENCE 217 AA; 25839 MW; AIEE3938F590B829 CRC64;
 SQ

Query Match Similarity 70.6%; Score 36; DB 1; Length 217;
 Best Local Similarity 85.7%; Pred. No. 9.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPNAPYL 9
 56 PPNAPYL 62

RESULT 11
 GTM1 RAT STANDARD; PRT; 217 AA.
 AC P04905;
 DT 13-AUG-1987 (Rel. 05, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glutathione S-transferase Yb1 (EC 2.5.1.18) (Chain 3) (GST M1-1)
 DE (GST class-mu 1).
 GN GSTM1.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 CX [1]
 RP SEQUENCE FROM N.A. (CLONE PGTR200).
 RP MEDLINE=86312882; Pubmed=2875437;
 RA Lai H.-C.J., Grove G., Tu C.-P.D.;
 RT "Cloning and sequence analysis of a cDNA for a rat liver glutathione
 RT S-transferase Yb subunit.";
 RL Nucleic Acids Res. 14:6101-6114(1986).
 RN [2]
 RP SEQUENCE FROM N.A. (CLONE PGTA/C44).
 RP MEDLINE=86033768; Pubmed=3840477;
 RA Ding G.J.-F., Lu A.Y.H., Pickett C.B.;
 RT "Rat liver glutathione S-transferases. Nucleotide sequence analysis
 RT of a Yb1 cDNA clone and prediction of the complete amino acid
 RT sequence of the Yb1 subunit.";
 RL J. Biol. Chem. 260:13268-13271(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=86224097; Pubmed=3011803;
 RA Ding G.J.-F., Ding V.D.-H., Rodkey J.A., Bennett C.D., Lu A.Y.H.,
 RA Pickett C.B.;
 RT "Rat liver glutathione S-transferases. DNA sequence analysis of a Yb2
 RT cDNA clone and regulation of the Yb1 and Yb2 mRNAs by
 RT phenobarbital.";
 RL J. Biol. Chem. 261:7952-7957(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=87308179; Pubmed=3040722;
 RA Chang C., Saltzman A.G., Sorensen N.S., Hilpakka R.A., Liao S.;
 RT "Identification of glutathione S-transferase Yb1 mRNA as the
 RT androgen-repressed mRNA by cDNA cloning and sequence analysis.";
 RL J. Biol. Chem. 262:11901-11903(1987).
 RN [5]
 RP SEQUENCE OF 1-23.
 RP STRAIN=Mistar; TISSUE=Olfactory epithelium;
 RP MEDLINE=93277499; Pubmed=8503873;
 RA Ben-Arie N., Khen M., Lancel D.;
 RT "Glutathione S-transferases in rat olfactory epithelium:
 RT purification, molecular properties and odorant biotransformation.";
 RL Biochem. J. 292:379-384(1993).
 RN [6]
 RP MUTAGENESIS OF CYS-86.
 RP MEDLINE=91354218; Pubmed=1883338;
 RA Hsieh J.-C., Huang S.-C., Chen W.-L., Lai Y.-C., Tam M.F.;
 RT "Cysteine-86 is not needed for the enzymic activity of glutathione S-
 RT transferase 3-3.";
 RL Biochem. J. 278:293-297(1991).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RP MEDLINE=93041702; Pubmed=1420139;
 RA Ji X., Zhang P., Armstrong R.N., Gilliland G.L.;
 RT "The three-dimensional structure of a glutathione S-transferase from
 RT the mu gene class. Structural analysis of the binary complex of
 RT isoenzyme 3-3 and glutathione at 2.2-A resolution.";
 RL Biochemistry 31:10169-10184(1992).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RA Fu J.-H., Rose J., Tam M.F., Wang B.-C.;
 RT "New crystal forms of a mu-class glutathione S-transferase from rat
 RT liver.";
 RL Acta Crystallogr. D 50:219-224(1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RP MEDLINE=94153886; Pubmed=8110735;
 RA Ji X., Johnson W.W., Sesay M.A., Dickert L., Prasad S.M., Ammon H.L.,

RA Armstrong R.N., Gilliland G.L.;
 RT "Structure and function of the xenobiotic substrate binding site of a
 RT glutathione S-transferase as revealed by X-ray crystallographic
 RT analysis of product complexes with the diastereomers of 9-(S-
 RT glutathionyl)-10-hydroxy-9,10-dihydrophenanthrene.";
 RL Biochemistry 33:1043-1052(1994).
 CC -1- FUNCTION: CATABOLISM OF REDUCED GLUTATHIONE TO A WIDE NUMBER
 CC OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
 CC -1- FUNCTION: THE OLFACTORY GST MAY BE CRUCIAL FOR THE ACTIVITY OF THE
 CC OLFACTORY PROCESS.
 CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOSOL.
 CC -1- MISCELLANEOUS: RAT LIVER GLUTATHIONE S-TRANSFERASES (GST) CONSIST
 CC OF BINARY COMBINATIONS OF THREE MAJOR CLASSES OR SUBUNITS
 CC DESIGNATED: YA (25 KDA), YB (27 KDA) AND YC (28 KDA).
 CC -1- MISCELLANEOUS: YB SUBCLASS SELECTIVELY BINDS STEROID HORMONES.
 CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY.
 CC -----
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 CC -----
 CC EMBL; X04229; CAA27811.1; -;
 CC EMBL; M11719; AAA41287.1; -;
 CC EMBL; J02810; AAA41293.1; -;
 CC PIR; A29794; A29794.
 DR PDB; 1G8B; 31-OCT-93.
 DR PDB; 1G8C; 31-OCT-93.
 DR PDB; 2G8T; 31-OCT-93.
 DR PDB; 3G8T; 31-JAN-94.
 DR PDB; 4G8T; 31-OCT-93.
 DR PDB; 5G8T; 31-OCT-93.
 DR PDB; 6G8T; 08-NOV-96.
 DR PDB; 6GSU; 08-NOV-96.
 DR PDB; 6GSV; 08-NOV-96.
 DR PDB; 6GSW; 08-NOV-96.
 DR PDB; 6GSX; 08-NOV-96.
 DR PDB; 6GSY; 08-NOV-96.
 DR PDB; 5FNG; 27-JAN-99.
 DR PDB; 3FYG; 01-JUN-99.
 DR InterPro; IPR004046; GST_Cterm.
 DR InterPro; IPR001081; GST_mu.
 DR InterPro; IPR004045; GST_Nterm.
 DR Pfam; PR00043; GST_C; 1.
 DR Pfam; PR02798; GST_N; 1.
 DR PRINTS; PR01267; GSTRNSPASEM.
 DR TRANSFERASE; Multigene family; 3D-structure; Olfaction.
 KW INT MET
 FT MUTAGEN 86 86
 FT INT MET 168 168
 FT CONFLICT 198 199
 FT STRAND 2 7
 FT TURN 11 13
 FT HELIX 14 22
 FT TURN 23 24
 FT STRAND 27 32
 FT TURN 37 39
 FT HELIX 43 46
 FT TURN 47 48
 FT HELIX 49 51
 FT STRAND 61 64
 FT TURN 65 66
 FT STRAND 67 70
 FT HELIX 72 82
 FT TURN 83 84
 FT HELIX 90 114
 FT TURN 115 115
 FT TURN 117 118
 C-S: NO CHANGE IN ACTIVITY.
 I -> N (IN REF. 3).
 KS -> NC (IN REF. 2).

FT HELIX 119 128
 FT TURN 129 129
 FT HELIX 130 141
 FT TURN 142 143
 FT HELIX 154 166
 FT TURN 171 176
 FT HELIX 178 188
 FT TURN 189 189
 FT HELIX 191 197
 FT TURN 198 198
 FT TURN 200 201
 FT TURN 210 211
 FT TURN 217 AA; 25782 MW; 2ACE8D49DA785118 CRC64;
 SO SEQUENCE 217 AA; 25782 MW; 2ACE8D49DA785118 CRC64;
 Query Match 70.6%; Score 36; DB 1; Length 217;
 Best Local Similarity 85.7%; Pred. No. 9.4;
 Matches 6; Conservative. 0; Mismatches 1; Indels 0; Gaps 0;

Gy 3 PPNAPYL 9
 Db 56 PPNAPYL 62

RESULT 12
 GTM2_HUMAN STANDARD; PRT; 217 AA.
 ID GTM2_HUMAN STANDARD; PRT; 217 AA.
 AC P28161_Q8MWE1; Rel. 25; Created)
 DT 01-APR-1993 (Rel. 25; Last sequence update)
 DT 01-APR-1993 (Rel. 25; Last annotation update)
 DE 15-SEP-2003 (Rel. 42; Last annotation update)
 DE Glutathione S-transferase Mu 2 (EC 2.5.1.18) (GSTM2-2) (GST class-mu 2)
 GN GSTM2 OR GST4
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RC MEDLINE=91239584; Pubmed=2034681;
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Alexander S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carrincci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs S.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [3]
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
 RA MEDLINE=94238693; Pubmed=8182750;
 RA Ragunathan S., Chandross R.J., Kretzinger R.H., Allison T.J.,

RA Penington C.J., Rule G.S.;
 RT "Crystal structure of human class mu glutathione transferase GSTM2-2.
 RT Effects of lattice packing on conformational heterogeneity."; J.
 RL J. Mol. Biol. 238:815-832(1994).
 CC -1- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER
 CC OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
 CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: THIS IS A MUSCLE ISOZYME.
 CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY.
 CC -----
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 CC -----
 CC EMBL; M63509; AAA60963.1; -;
 DR EMBL; BC017836; AAH17836.1; -;
 DR PIR; A39375; A39375.
 DR PDB; 1HNA; 31-JAN-94.
 DR PDB; 1HNB; 31-JAN-94.
 DR PDB; 1HNC; 31-JAN-94.
 DR PDB; 2GTU; 02-MAR-99.
 DR PDB; 3GTU; 28-JUL-99.
 DR GeneW; HGNC:4634; GSTM2.
 DR MIM; 138380; -;
 DR GO; GO:0004364; F:glutathione transferase activity; TAS.
 DR InterPro; IPR004046; GST_Cterm.
 DR InterPro; IPR003081; GST_mu.
 DR InterPro; IPR004045; GST_Nterm.
 DR Pfam; PF00045; GST_C; 1.
 DR Pfam; PF02798; GST_N; 1.
 DR PRINTS; PR01267; GSTRNMFRASEM.
 DR Transferrase; Multigene family; 3D-structure.
 KW INIT MET
 FT FT 0
 FT INIT MET 0
 FT CONFLICT 189 217 GLEKISAYMKSSRRLPPVPTKVAWGK -> EKCNVGMSS
 FT STRAND 2 7 SRRMLDVTVCRTSRIILQCNBENE (IN REF. 2).
 FT HELIX 11 13
 FT HELIX 14 22
 FT TURN 23 24
 FT TURN 27 28
 FT STRAND 32 32
 FT HELIX 43 46
 FT HELIX 47 51
 FT TURN 49 49
 FT STRAND 61 64
 FT TURN 65 66
 FT STRAND 67 70
 FT HELIX 82 84
 FT HELIX 85 88
 FT TURN 90 90
 FT HELIX 112 112
 FT TURN 113 114
 FT HELIX 119 141
 FT TURN 142 143
 FT STRAND 146 146
 FT TURN 147 148
 FT STRAND 149 149
 FT HELIX 154 169
 FT HELIX 171 175
 FT TURN 176 176
 FT HELIX 178 188
 FT TURN 189 189
 FT HELIX 191 198
 FT TURN 200 201
 FT TURN 207 211
 FT TURN 214 215
 FT TURN 217 AA; 25613 MW; 25603A909482CA39 CRC64;
 SO SEQUENCE 217 AA; 25613 MW; 25603A909482CA39 CRC64;
 Query Match 70.6%; Score 36; DB 1; Length 217;

Best Local Similarity 85.7%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 PPNAPYL 9
Db 56 PPNLPLYL 62

RESULT 13

GM2_MOUSE STANDARD; PRT; 217 AA.
AC P15626;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutathione S-transferase Mu 2 (EC 2.5.1.18) (GST class-mu 2)
GN GSTM2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

SEQUENCE FROM N.A.
RX MEDLINE=90094327; Pubmed=2689439;
RA Townsend A.J., Goldsmith M.E., Pickett C.B., Cowan K.H.;
RT "Isolation, characterization, and expression in Escherichia coli of
RT two murine Mu class glutathione S-transferase cDNAs homologous to the
RT rat subunits 3 (Yb1) and 4 (Yb2).";
RL J. Biol. Chem. 264:21582-21590(1989).
RN [2]

SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=21297196; Pubmed=11404019;
RA Kumar A., Reddy E.P.;
RT "Genomic organization and characterization of the promoter region of
RT murine GSTM2 gene.";
RL Gene 270:221-229(2001).
RN [1]

-1- FUNCTION: CONTIGUATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER
OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
-1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
-1- SUBUNIT: Homodimer.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY.

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EMBL; J04696; AAA37706.1; -.
EMBL; AF19526; AAK8508.1; -.
PIR; B34159; B34159.
HSSP; P09489; 1GTU.
DR SWISS-2DPAGE; P15626; MOUSE.
DR MGD; MGI:95861; Gstm2.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR003081; GST_mu.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
DR PRINTS; PR01267; GSTNSFRASEM.
KW Transferase; Multigene family.
FT INT MET 0
SQ SEQUENCE 217 AA: 25585 MW; A3979D4435FF08AE CRC64;

Query Match 70.6%; Score 36; DB 1; Length 217;
Best Local Similarity 85.7%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 PPNAPYL 9
Db 56 PPNLPLYL 62

RESULT 14

GM2_RAT STANDARD; PRT; 217 AA.
AC P0810;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutathione S-transferase Yb2 (EC 2.5.1.18) (Chain 4) (GST class-mu
DE 2)
GN GSTM2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

SEQUENCE FROM N.A.
RX MEDLINE=88298790; Pubmed=3403534;
RA Lai H.-C.J., Qian B., Grove G., Tu C.-P.D.;
RT "Gene expression of rat glutathione S-transferases. Evidence for gene
RT conversion in the evolution of the Yb multigene family.";
RL J. Biol. Chem. 263:11389-11395(1988).
RN [2]

SEQUENCE:
RA STRAIN=Sprague-Dawley;
RX MEDLINE=86192461; Pubmed=3699019;
RA Alin P., Mannervik B., Joernvall H.;
RT "Cytosolic rat liver glutathione transferase 4-4. Primary structure
RT of the protein reveals extensive differences between homologous
RT glutathione transferases of classes alpha and mu.";
RL Eur. J. Biochem. 156:343-350(1986).
RN [3]

SEQUENCE OF 24-217 FROM N.A.
RX MEDLINE=86224097; Pubmed=3011803;
RA Ding G.-J., Ding V.D.-H., Rodkey J.A., Bennett C.D., Lu A.Y.H.,
RA Pickett C.B.;
RT "Rat liver glutathione S-transferases. DNA sequence analysis of a Yb2
RT cDNA clone and regulation of the Yb1 and Yb2 mRNAs by
RT phenobarbital.";
RL J. Biol. Chem. 261:7952-7957(1986).
RN [4]

SEQUENCE OF 32-217 FROM N.A.
RX MEDLINE=87008619; Pubmed=3020050;
RA Lai H.-C.J., Tu C.-P.D.;
RT "Rat glutathione S-transferases supergene family. Characterization of
RT an amionic Yb subunit cDNA clone";
RL J. Biol. Chem. 261:13793-13799(1986).
RN [5]

SEQUENCE OF 1-21.
RA STRAIN=wislar; TISSUE=Olfactory epithelium;
RX MEDLINE=93277499; Pubmed=8503873;
RA Ben-Arie N., Khem M., Lancel D.;
RT "Glutathione S-transferases in rat olfactory epithelium:
RT purification, molecular properties and odorant biotransformation.";
RL Biochem. J. 292:379-384(1993).
CC -1- FUNCTION: CONTIGUATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER
CC OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
CC -1- FUNCTION: THE OLFACTORY GST MAY BE CRUCIAL FOR THE ACTIVITY OF THE
CC OLFACTORY PROGRESS.
CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -1- SUBUNIT: HOMODIMER OR HETERODIMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MSCLELLULAR LOCATION: Cytoplasmic.
CC OF BINARY COMBINATIONS OF THREE MAJOR CLASSES OF SUBUNITS
CC DESIGNATED: YA (25 KDA), YB (27 KDA) AND YC (28 KDA).
CC -1- MISCELLANEOUS: YB SUBCLASS SELECTIVELY BINDS STEROID HORMONES.
CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY.

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EMBL; J02592; AAA41285.1; -
 EMBL; M13590; AAA42351.1; -
 EMBL; J03914; AAA41296.1; -
 PIR; A29231; XURTG4.
 HSSP; P09488; 1GTU.
 InterPro; IPR004046; GST_Cterm.
 InterPro; IPR004045; GST_Nterm.
 Pfam; PF00043; GST_C; 1.
 Pfam; PF02798; GST_N; 1.
 Transferrase; Multigene family; Olfaction.
 INIT MET 0
 COMPACT 0
 SEQUENCE 217 AA; 25571 MW; F27B3D5831FF789F CRC64;

Query Match 70.6%; Score 36; DB 1; Length 217;
 Best Local Similarity 85.7%; Pred. No. 9.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPNAPYL 9
 DB 56 PPNLPEYL 62

RESULT 15
 GFM3_MOUSE STANDARD; PRT; 217 AA.
 ID GFM3_MOUSE P19639;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glutathione S-transferase Mu 3 (EC 2.5.1.18) (GST class-mu 3)
 DE (Glutathione S-transferase G9.3).
 GN GSTM3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88330838; PubMed=3417659;
 RA Pearson W.R., Reinhardt J., Siek S.C., Anderson K.S., Adler P.N.;
 RT "Tissue-specific induction of murine glutathione transferase mRNAs by
 butylated hydroxyanisole."
 RL J. Biol. Chem. 263:13324-13332(1988).
 RN [2]
 RP SEQUENCE OF 1-40 FROM N.A.
 RX MEDLINE=83109018; PubMed=6822548;
 RA Pearson W.R., Windle J.T., Morrow J.F., Benson A.M., Talalay P.;
 RT "Increased synthesis of glutathione S-transferases in response to
 anticarcinogenic antioxidants. Cloning and measurement of messenger
 RNA."
 RL J. Biol. Chem. 258:2052-2062(1983).
 RN [3]
 RP SEQUENCE OF 1-25.
 RX MEDLINE=86042634; PubMed=3864155;
 RA Mannervik B., Alin P., Guttenberg C., Jansson H., Tahir M.K.,
 Watholm M., Joernvall H.;
 RT "Identification of three classes of cytosolic glutathione transferase
 common to several mammalian species: correlation between structural
 data and enzymatic properties."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7202-7206(1985).
 RU -1- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER
 CC OF XENOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
 CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

-1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY.
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 or send an email to license@isb-sib.ch).

EMBL; J03953; AAA37748.1; ALT_INIT.
 PIR; B28946; B28946.
 HSSP; P04905; 2GST.
 MGD; MGI:106026; Gatm3.
 InterPro; IPR004046; GST_Cterm.
 InterPro; IPR003081; GST_mu.
 InterPro; IPR004045; GST_Nterm.
 Pfam; PF00043; GST_C; 1.
 Pfam; PF02798; GST_N; 1.
 PRINTS; PR01267; GSTNSPFRASEM.
 Transferrase; Multigene family.
 INIT MET 0
 COMPACT 0
 SEQUENCE 217 AA; 25570 MW; C4D8950EFEA585D8 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 217;
 Best Local Similarity 85.7%; Pred. No. 9.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPNAPYL 9
 DB 56 PPNLPEYL 62

Search completed: January 21, 2004, 08:45:07
 Job time : 12 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 21, 2004, 08:36:24 ; Search time 35 Seconds
(Without alignments)
66.356 Million cell updates/sec

Title: US-09-625-963A-1
Perfect score: 51
Sequence: 1 RMPNPAPYL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP_archaea:*
- 2: SP_bacteria:*
- 3: SP_fungi:*
- 4: SP_human:*
- 5: SP_invertebrate:*
- 6: SP_mammal:*
- 7: SP_mhc:*
- 8: SP_organelle:*
- 9: SP_phase:*
- 10: SP_plant:*
- 11: SP_rodent:*
- 12: SP_virus:*
- 13: SP_vertebrate:*
- 14: SP_unclassified:*
- 15: SP_virus:*
- 16: SP_bacteriap:*
- 17: SP_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	407	13 P79958	P79958 xenopus lae
2	51	100.0	446	4 O15881	O15881 homo sapien
3	47	92.2	390	13 O42223	O42223 trachemys s
4	47	84.3	386	13 O90XX8	O90XX8 oncorhynch
5	43	84.3	388	13 O90XX7	O90XX7 oncorhynch
6	43	84.3	409	13 O91657	O91657 xenopus lae
7	43	84.3	417	13 O90XX6	O90XX6 oncorhynch
8	41	80.4	213	16 O929M3	O929M3 listeria in
9	41	80.4	213	16 O8Y5B7	O8Y5B7 listeria in
10	40	78.4	250	13 O985T4	O985T4 brachydanio
11	40	78.4	289	16 O8XPE7	O8XPE7 talponta s
12	40	78.4	392	13 O91030	O91030 gallus gall
13	40	78.4	414	13 O918A1	O918A1 gallus gall
14	40	78.4	417	13 O918A0	O918A0 gallus gall
15	40	78.4	419	13 O9PUT7	O9PUT7 brachydanio
16	39	76.5	203	16 O83076	O83076 treponema p

ID	WTI	WTI protein	WTI	WTI protein	WTI	WTI protein	WTI	WTI protein	WTI	WTI protein
17	39	76.5	392	13 O91BF0	O91BF0 anguilla ja					
18	39	76.5	426	13 O9W611	O9W611 cynops pyr					
19	38	74.5	205	16 O91AD6	O91AD6 pseudomona					
20	38	74.5	214	16 O8TSH2	O8TSH2 anabaena sp					
21	38	74.5	410	13 O8UIR9	O8UIR9 oryzaia lat					
22	38	74.5	581	10 O9FZ97	O9FZ97 arabidopsis					
23	38	74.5	581	10 O8W4K7	O8W4K7 arabidopsis					
24	38	74.5	662	5 O9N6S5	O9N6S5 leishmania					
25	38	74.5	966	5 O961M6	O961M6 drosophila					
26	38	74.5	2175	5 O9W198	O9W198 drosophila					
27	37	72.5	183	16 O8D9S3	O8D9S3 vdr10 vulin					
28	37	72.5	444	10 O91LS41	O91LS41 arabidopsis					
29	37	72.5	541	3 O8TGS25	O8TGS25 aspergillus					
30	37	72.5	1160	4 O8TND24	O8TND24 homo sapien					
31	36	70.6	32	11 O9QVM0	O9QVM0 mus sp. gju					
32	36	70.6	37	11 O9QVM3	O9QVM3 mus sp. gju					
33	36	70.6	62	10 O8GSM0	O8GSM0 triticum ae					
34	36	70.6	62	10 O8GSL8	O8GSL8 triticum ae					
35	36	70.6	82	4 O9UE37	O9UE37 homo sapien					
36	36	70.6	118	4 O96BP2	O96BP2 homo sapien					
37	36	70.6	181	4 O8TCS98	O8TCS98 homo sapien					
38	36	70.6	188	6 O9WZB4	O9WZB4 capra hircu					
39	36	70.6	195	4 O05465	O05465 homo sapien					
40	36	70.6	218	6 O9TSM4	O9TSM4 macaca fasc					
41	36	70.6	218	6 O9NOV4	O9NOV4 bos taurus					
42	36	70.6	218	6 O9TSM5	O9TSM5 macaca fasc					
43	36	70.6	218	11 O91YB3	O91YB3 cavia porce					
44	36	70.6	218	11 O8RS16	O8RS16 mus musculu					
45	36	70.6	218	11 O8K0C3	O8K0C3 mus musculu					

ALIGNMENTS

RESULT 1
P79958 PRELIMINARY; PRT; 407 AA.
AC P79958;
DT 01-MAY-1997 (TRMBLrel. 03, Created)
DT 01-MAY-1997 (TRMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
DE WTI protein.
GN WTI.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Piploidea;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=97074667; PubMed=8917094;
RA Samba K., Salto-Ueno R., Takayama G., Kondo M.;
RT "cDNA cloning and its promoter-specific expression of the Wilms'
RT tumor suppressor gene, WTI, from Xenopus laevis.";
RL Gene 175;167-172(1996).
DR EMBL; D82051; BA011522.1; -;
DR HSSP; P08046; IAAV.
DR InterPro; IPR000976; Wilms tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PR02165; WTI_1.
DR Pfam; PR00096; ZF_C2H2_4.
DR PRINTS; PR00049; WILMSTUMOUR.
DR PRODOM; PD000003; Znf_C2H2_2.
DR SMART; SM00355; Znf_C2H2_4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PSS0157; ZINC_FINGER_C2H2_2; 4.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 407 AA; 45983 MW; E2554C658005870C CRC64;
Query Match 100.0%; Score 51; DB 13; Length 407;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
 Db 107 RMPFNAPYL 115

RESULT 2
 Q15881 PRELIMINARY; PRT; 446 AA.

AC Q15881;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Wilms tumor gene 1, exon 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92241883; PubMed=1572653;
 RA Gessler M., Konig A., Bruns G.A.;
 RT "The genomic organization and expression of the WT1 gene.";
 RL Genomics 12:807-813(1992).
 DR EMBL; X61631; CAA43819.1; -;
 DR EMBL; X61632; CAA43819.1; JOINED.
 DR EMBL; X61633; CAA43819.1; JOINED.
 DR EMBL; X61634; CAA43819.1; JOINED.
 DR EMBL; X61635; CAA43819.1; JOINED.
 DR EMBL; X61636; CAA43819.1; JOINED.
 DR EMBL; X61637; CAA43819.1; JOINED.
 DR EMBL; X61638; CAA43819.1; JOINED.
 DR HSSP; P08046; 1AAY.
 DR InterPro; IPR000976; Wilms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WT1; 1.
 DR Pfam; PF00096; zf-C2H2; 4.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR PRODOM; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 446 AA; 48842 MW; 8CE7FC047P41CFL1 CRC64;

Qy 1 RMPFNAPYL 9
 Db 126 RMPFNAPYL 134

RESULT 3
 O42223 PRELIMINARY; PRT; 390 AA.

AC O42223;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Wilms tumor 1 protein.
 GN WT1.
 OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.
 OX NCBI_TaxID=34903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Spocilla L.D., Hall S.E.;
 RT "Expression of a new RNA-splice isoform of WT1 in developing kidney/gonadal complexes of the turtle, Trachemys scripta.";
 RT Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF019779; AAB70832.1; -;
 DR HSSP; P08046; 1AAY.
 DR InterPro; IPR000976; Wilms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WT1; 1.
 DR Pfam; PF00096; zf-C2H2; 4.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR PRODOM; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 390 AA; 43620 MW; 1C9987435BB927C2 CRC64;

Qy 1 RMPFNAPYL 9
 Db 109 RMPFNAPYL 117

RESULT 4
 Q90XX8 PRELIMINARY; PRT; 386 AA.

AC Q90XX8;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Wilms' tumor suppressor 1a.
 GN WT-TLA.
 OS Oncorhynchus mykiss (rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Procaranchopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21337607; PubMed=11444705;
 RA Brantley J.P., Robison B.D., Thorgaard G.H.;
 RT "Ancient and recent duplications of the rainbow trout Wilms' tumor gene.";
 RL Genome 44:455-462(2001).

DR EMBL; AF334670; AKRS2719.1; -;
 DR InterPro; IPR000976; Wilms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WT1; 1.
 DR Pfam; PF00096; zf-C2H2; 4.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR PRODOM; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 386 AA; 43286 MW; 05622EF7642FC9B5 CRC64;

Qy 1 RMPFNAPYL 9
 Db 112 RMPFNAPYL 120

RESULT 5
 Q90XX7 PRELIMINARY; PRT; 388 AA.

AC Q90XX7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Wlms' tumor suppressor 1b.
 GN WT-T1B
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RK MEDLINE=21337607; PubMed=11444705;
 RA Brunelli J.P., Robison B.D., Thorgaard G.H.;
 RT "Ancient and recent duplications of the rainbow trout Wlms' tumor
 gene";
 RL Genome 44:455-462(2001).
 DR EMBL; AF334671; AAKS2720.1; -
 DR InterPro; IPR000976; Wlms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WTI; 1.
 DR Pfam; PF00096; zf-C2H2; 4.
 DR Pfam; PF00003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 KM Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 388 AA; 43398 MW; BC92266DE745DFCC CRC64;
 QY Query Match 84.3%; Score 43; DB 13; Length 388;
 Best Local Similarity 88.9%; Pred. No. 4.6;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 RMPFNAPYL 9
 Db 112 RMPFNAPYL 120
 RESULT 6
 Q91657 PRELIMINARY; PRT; 409 AA.
 AC Q91657;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Wlms' tumor suppressor (WT1).
 GN WTI.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 CC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RK Carroll T.J., Vize P.D.;
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 289-370 FROM N.A.
 RC TISSUE=Meonephros;
 RX MEDLINE=96068905; PubMed=7478606;
 RA Kent J., Coriat A.M., Sharpe P.T., Hastie N., Van Heyningen V.;
 RT "The evolution of WTI sequence and expression pattern in the
 vertebrates";
 RL Oncogene 11:1781-1792(1995).
 DR EMBL; U42011; AAB53152.1; -
 DR EMBL; X85733; CA59738.1; -
 DR HSSP; P08046; IAAV.
 DR InterPro; IPR000976; Wlms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00165; WTI; 1.
 DR Pfam; PF00096; zf-C2H2; 4.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR PRODOM; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 RA PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.

KM Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 409 AA; 46186 MW; 2217FC04612CDE10 CRC64;
 QY Query Match 84.3%; Score 43; DB 13; Length 409;
 Best Local Similarity 88.9%; Pred. No. 4.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 RMPFNAPYL 9
 Db 106 RMPFNAPYL 114
 RESULT 7
 Q90XX6 PRELIMINARY; PRT; 417 AA.
 AC Q90XX6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Wlms' tumor suppressor 1b variant.
 GN WT-T1B.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RK MEDLINE=21337607; PubMed=11444705;
 RA Brunelli J.P., Robison B.D., Thorgaard G.H.;
 RT "Ancient and recent duplications of the rainbow trout Wlms' tumor
 gene";
 RL Genome 44:455-462(2001).
 DR EMBL; AF334672; AAKS2721.1; -
 DR InterPro; IPR000976; Wlms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WTI; 1.
 DR Pfam; PF00096; zf-C2H2; 4.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR PRODOM; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 KM Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 417 AA; 46557 MW; 5217620CD471D030 CRC64;
 QY Query Match 84.3%; Score 43; DB 13; Length 417;
 Best Local Similarity 88.9%; Pred. No. 4.9;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 RMPFNAPYL 9
 Db 112 RMPFNAPYL 120
 RESULT 8
 Q929M3 PRELIMINARY; PRT; 213 AA.
 AC Q929M3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein lin2252.
 GN LIN2252.
 OS Listeria innocua.
 CC Bacteria; Firmicutes; Bacilliales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RK STRAIN=CLIP 11262 / Serovar 6a;
 RX PubMed=11679669;
 RA Glaser P., Franzen L., Buchrieser C., Ruenjok C., Amend A.,
 Baquero F., Berche P., Bioecker H., Brandt P., Chakraborty T.,

RA Charbit A., Cherouani F., Couve E., de Daruvar A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido F.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kuntz F., Kurapkak G.,
 RA Madeno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Rammel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of *Listeria species*.";
 RL Science 294:849-852(2001).
 DR EMBL: AL596171; CAC97480.1; -
 DR Listlist: LIT02252; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 213 AA; 25341 MW; B87F90FD1D1F0E78 CRC64;

Query Match 80.4%; Score 41; DB 16; Length 213;
 Best Local Similarity 100.0%; Pred. No. 5.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 FPNAPYL 9
 Db 67 FPNAPYL 73

RESULT 9
 O8Y5B7 PRELIMINARY; PRT; 213 AA.

AC O8Y5B7;
 DT 01-MAR-2002 (TRMBLrel. 20, Created)
 DT 01-MAR-2002 (TRMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TRMBLrel. 20, Last annotation update)
 DE Hypothetical protein Imo2148.
 GN LMO2148.
 OS *Listeria monocytogenes*.
 OC Bacteria; Firmicutes; Bacillales; *Listeriaceae*; *Listeria*.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-e / Serovar 1/2a;
 RC MEDLINE=21537279; PubMed=11679669;
 RA Glaeser P., Frangaul L., Buchrieser C., Rusniok C., Amend A.,
 RA Banquer F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Chabibo A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido F.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kuntz F., Kurapkak G.,
 RA Madeno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Rammel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of *Listeria species*.";
 RL Science 294:849-852(2001).
 DR EMBL: AL591982; CAD00226.1; -
 DR Listlist: LMO2148; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 213 AA; 25361 MW; A9BF9363E2F0E78 CRC64;

Query Match 100.4%; Score 41; DB 16; Length 213;
 Best Local Similarity 100.0%; Pred. No. 5.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 FPNAPYL 9
 Db 67 FPNAPYL 73

RESULT 10
 O98S34 PRELIMINARY; PRT; 250 AA.
 AC O98S34;
 DT 01-JUN-2001 (TRMBLrel. 17, Created)

DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
 DE Mims' tumor suppressor (Fragment).
 GN WTL.
 OS *Brychodanio rerio* (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Serluca F.C., Fishman M.C.;
 RT "Pre-pattern in the pronephric kidney field of zebrafish.";
 RL Development 0:0-0(2001).
 DR EMBL: AY028627; AAK27262.1; -
 DR ZFIN; ZDB-GENE-980526-558; WTL.
 DR InterPro; IPR000976; Wlms_tumour.
 DR Pfam; PF02165; WTL1; 1.
 FT NON_TER 1 1
 FT NON_TER 250 250
 SQ SEQUENCE 250 AA; 27236 MW; 90FA4B05FF59FEA CRC64;

Query Match 78.4%; Score 40; DB 13; Length 250;
 Best Local Similarity 77.8%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MFPPNAPYL 9
 Db 88 RMFNSPYL 96

RESULT 11
 O8XP67 PRELIMINARY; PRT; 289 AA.

AC O8XP67;
 DT 01-MAR-2002 (TRMBLrel. 20, Created)
 DT 01-MAR-2002 (TRMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TRMBLrel. 20, Last annotation update)
 DE Hypothetical lipoprotein transmembrane protein Rsp1673.
 GN RSP1673 OR R502232.
 OS *Ralstonia solanacearum* (Pseudomonas solanacearum).
 OC Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; *Ralstonia*.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GMI1000;
 RC MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billault A., Brottier P., Camus J.C., Catalioco L.,
 RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaepin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Sigvier P., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*.";
 RL Nature 415:497-502(2002).
 DR EMBL: AL646086; CAD18824.1; -
 DR KW Plasmid; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 289 AA; 29665 MW; 7158677B3C03C9BC CRC64;

Query Match 78.4%; Score 40; DB 16; Length 289;
 Best Local Similarity 87.5%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 MFPPNAPYL 9
 Db 115 MLPPNAPYL 122

RESULT 12
 O91030 PRELIMINARY; PRT; 392 AA.
 ID O91030

AC 091030;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Chick Wilm's tumour protein (Fragment).
 GN CMT1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=96068905; PubMed=7478606;
 RA Kent J., Coriat A.M., Sharpe P.T., Hastle N., van Heyningen V.;
 RT "The evolution of WT1 sequence and expression in the vertebrates";
 RL Oncogene 11:1781-1792(1995).
 DR EMBL; X85731; CAAS9736.1; -.
 DR HSSP; P08046; 1AIG.
 DR InterPro; IPR000976; WILMS_tumour.
 DR InterPro; IPR07087; Znf_C2H2.
 DR Pfam; PF02165; WT1; 1.
 DR Pfam; PF00096; zf-C2H2; 3.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR PRODOM; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 3.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
 KM Metal-binding; Zinc; zinc-finger.
 FT NOW TRS 392 392
 SQ SEQUENCE 392 AA; 43869 MW; 761F01D350E4EDBF CRC64;
 QY
 Query Match 78.4%; Score 40; DB 13; Length 392;
 Best Local Similarity 77.8%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

KM Metal-binding; Zinc; zinc-finger.
 SQ SEQUENCE 414 AA; 46641 MW; 17B822F9B428A2EF CRC64;
 QY
 Query Match 78.4%; Score 40; DB 13; Length 414;
 Best Local Similarity 77.8%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 14
 0918A0 PRELIMINARY; PRT; 417 AA.
 AC 0918A0;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE WT1(+KTS) protein.
 GN WT1(+KTS).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Kido T.;
 RT "Chicken counterpart of Wilms' tumor suppressor gene 1.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB033634; BAA94794.1; -.
 DR HSSP; P08046; 1AAY.
 DR InterPro; IPR000976; WILMS_tumour.
 DR InterPro; IPR07087; Znf_C2H2.
 DR Pfam; PF02165; WT1; 1.
 DR Pfam; PF00096; zf-C2H2; 4.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR PRODOM; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 KM Metal-binding; Zinc; zinc-finger.
 SQ SEQUENCE 417 AA; 46957 MW; 47BBF7F6448E76C CRC64;
 QY
 Query Match 78.4%; Score 40; DB 13; Length 417;
 Best Local Similarity 77.8%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 15
 09P0T7 PRELIMINARY; PRT; 419 AA.
 AC 09P0T7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Wilms' tumor suppressor.
 GN WT1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 CC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith S.I., Down M., Power M., Boyd A.W.;
 RT "Isolation and characterization of a cDNA encoding zebrafish (Danio

RT reio) WT-1";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF144550; AAF0123.1; -.
 DR HSSP; P08046; 1AAY.
 DR ZFIN; ZDB-GENE-980526-558; WT1.
 DR InterPro; IPR000976; Wlms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WT1_1.
 DR Pfam; PF00996; ZF-C2H2; 4.
 DR PRINTS; PR00049; WLMSTUMOUR.
 DR ProDom; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR SMART; SM00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 DR Metal-binding; Zinc; Zinc-finger.
 KW SEQUENCE 419 AA; 46925 MW; 606ADFPDPA619EBCD CRC64;

Query Match 78.4%; Score 40; DB 13; Length 419;
 Best Local Similarity 77.8%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RMPFNAPYL 9
 |||:||||
 Db 111 RMFSNSPYL 119

Search completed: January 21, 2004, 08:44:10
 Job time : 37 secs

OS Homo sapiens.
 XX W0200026249-A1.
 XX 11-MAY-2000.
 XX 02-NOV-1999; 99WO-GB03572.
 XX 02-NOV-1999; 98GB-0023897.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Stausz HJ, Gao L;
 XX WPI; 2000-376123/32.
 XX Novel peptides comprising WT-1 and GATA-1 epitopes, their fragments or
 XX variants, useful as vaccines for cancer immunotherapy
 XX Claim 1; Page 74; 93pp; English.
 XX The present sequence is peptide epitope WT126-34, produced by WT1
 XX expressing cells and found at residues 126-134 of the WT1 protein, which
 XX is recognised by cytotoxic T lymphocytes. WT1 is aberrantly expressed in
 XX leukaemia, breast cancer, melanoma and ovarian cancer. The peptide can
 XX be used as a vaccine to stimulate the elimination, by cytotoxic T
 XX lymphocytes, of cancer cells aberrantly expressing WT1. In addition, the
 XX nucleic acid encoding the peptide may also be used in the same manner.
 XX Alternatively, the peptide may be used in vitro to produce activated
 XX cytotoxic T lymphocytes.
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 51; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 Db 1 RMPFNAPYL 9

RESULT 2
 AAY98670
 ID AAY98670 standard; Peptide; 9 AA.
 AC AAY98670;
 XX
 XX 31-JUN-2000 (first entry)
 DT
 XX WT1 derived immunogenic peptide SEQ ID NO:185.
 DE
 XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
 XX metastatic disease; mouse; human; Wilm's tumour; immune response;
 KW vaccine.
 KW
 XX Homo sapiens.
 OS
 XX W0200018795-A2.
 PN
 XX 06-APR-2000.
 PD
 XX 30-SEP-1999; 99WO-US22819.
 PF
 XX 30-SEP-1998; 98US-0164223.
 PR
 XX 25-MAR-1999; 99US-0276484.
 PA (CORI-) CORIXA CORP.
 PA (GAIG/) GAIGER A.
 PI Gajger A, Cheever M;
 XX

DR WPI; 2000-293107/25.
 XX Novel polypeptides comprising an immunogenic portion of a native WT1
 XX polypeptide, useful for inhibiting the development of malignant
 XX diseases associated with WT1 expression e.g. leukemia or cancer
 XX Claim 4; Page 171; 193pp; English.
 XX The present invention describes polypeptides (I) comprising an
 XX immunogenic portion of a native Wilm's Tumour gene product polypeptide,
 XX WT1, (or variants of the immunogenic portion retaining the ability to
 XX react with WT1-specific antisera and/or T-cell lines or clones) and
 XX comprising 16 consecutive amino acids (aa) or less of a native WT1
 XX polypeptide. The polypeptides are useful therapeutically and to
 XX manufacture medicaments for enhancing/inducing an immune response in
 XX patients. The polypeptides, mimetics or polynucleotides can be included
 XX with a carrier/excipient in pharmaceutical compositions or with a
 XX non-specific immune response enhancer (e.g. an adjuvant or enhancer
 XX preferentially enhancing a T cell response) in vaccines. Pharmaceutical
 XX compositions and vaccines can be administered to human patients to
 XX enhance or induce an immune response specific for WT1 or a cell
 XX expressing WT1, useful to inhibit the development of malignant diseases
 XX associated with WT1 expression, e.g. leukemia (especially acute/chronic
 XX myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
 XX breast, lung, thyroid or gastrointestinal cancer, or a melanoma).
 XX AAY98501 to AAY98811 represent polypeptide sequences, and AAA13848 to
 XX AAA13862 represent PCR primers, used in the exemplification of the
 XX present invention.
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 51; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 Db 1 RMPFNAPYL 9

RESULT 3
 AAY98778
 ID AAY98778 standard; Peptide; 9 AA.
 AC AAY98778;
 XX
 XX 31-JUN-2000 (first entry)
 DT
 XX WT1 derived immunogenic peptide SEQ ID NO:293.
 DE
 XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
 XX metastatic disease; mouse; human; Wilm's tumour; immune response;
 KW vaccine.
 KW
 XX Mus musculus.
 OS
 XX W0200018795-A2.
 PN
 XX 06-APR-2000.
 PD
 XX 30-SEP-1999; 99WO-US22819.
 PF
 XX 30-SEP-1998; 98US-0164223.
 PR
 XX 25-MAR-1999; 99US-0276484.
 PA (CORI-) CORIXA CORP.
 PA (GAIG/) GAIGER A.
 PI Gajger A, Cheever M;
 XX
 XX Novel polypeptides comprising an immunogenic portion of a native WT1
 XX

PT polypeptide, useful for inhibiting the development of malignant
 PT diseases associated with WT1 expression e.g. leukemia or cancer
 XX
 PS Claim 4, Page 186, 193pp; English.
 XX
 CC The present invention describes polypeptides (I) comprising an
 CC immunogenic portion of a native Wilms' Tumour gene product polypeptide,
 CC (or variants of the immunogenic portion retaining the ability to
 CC react with WT1-specific antibodies and/or T-cell lines or clones) and
 CC comprising 16 consecutive amino acids (aa) or less of a native WT1
 CC polypeptide. The polypeptides are useful therapeutically and to
 CC manufacture medicaments for enhancing/inducing an immune response in
 CC patients. The polypeptides, mimetics or polynucleotides can be included
 CC with a carrier/excipient in pharmaceutical compositions or with a
 CC non-specific immune response enhancer (e.g. an adjuvant or enhancer
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
 CC compositions and vaccines can be administered to human patients to
 CC enhance or induce an immune response specific for WT1 or a cell
 CC expressing WT1, useful to inhibit the development of malignant diseases
 CC associated with WT1 expression, e.g. leukemia (especially acute/chronic
 CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).
 CC AAY98501 to AAY98811 represent polypeptide sequences, and AAA13848 to
 CC AAA13862 represent PCR primers, used in the exemplification of the
 CC present invention.
 CC
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 51; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 RMPFNAPYL 9
 1 RMPFNAPYL 9
 1 RMPFNAPYL 9
 Db
 RESULT 4
 AAY80200
 ID AAY80200 standard; Peptide; 9 AA.
 XX
 AC AAY80200;
 XX
 DT 24-MAY-2000 (first entry)
 XX
 DE Human Wilms' tumour suppressor gene WT1 product peptide SEQ ID NO:5.
 XX
 KW Wilms' tumour suppressor gene; WT1; cancer; antigen; vaccine; MHC;
 KW major histocompatibility complex; leukaemia; tumour; antitumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200006602-A1.
 XX
 PD 10-FEB-2000.
 XX
 PF 30-JUL-1999; 99WO-JP04130.
 XX
 PR 31-JUL-1998; 98JP-0218093.
 XX
 PA (SUGI/) SUGIYAMA H.
 XX
 PI Sugiyama H, Oka Y;
 XX
 DR WPI; 2000-195264/17.
 XX
 PT Cancer antigens based on Wilms' tumor suppressor gene WT1 product or
 PT peptide derivatives; for cancer vaccines in treating leukemia and solid
 PT tumor e.g. stomach cancer, skin cancer, lung cancer and breast cancer
 XX
 PS Claim 5; Page 18; 48pp; Japanese.
 XX
 CC The present invention describes a cancer antigen containing the active

CC component of Wilms' tumour suppressor gene WT1 product, or partial
 CC peptides, for cancer vaccines in treating leukaemia and solid tumours.
 CC The cancer antigens are useful for cancer vaccines in treating
 CC leukaemia, bone-marrow abnormal formation syndrome, malignant lymphoma,
 CC multiple myeloma, stomach cancer, cancer of the large intestine, lung
 CC cancer, breast cancer, blastoma, liver cancer, skin cancer, bladder
 CC cancer, prostate cancer, uterus cancer, cervical cancer, or ovary
 CC cancer. The present sequence represents a peptide from the human
 CC Wilms' tumour suppressor gene WT1 product.
 XX
 SQ Sequence 9 AA;
 XX
 Query Match 100.0%; Score 51; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 RMPFNAPYL 9
 1 RMPFNAPYL 9
 1 RMPFNAPYL 9
 Db
 RESULT 5
 AAU68769
 ID AAU68769 standard; Peptide; 9 AA.
 XX
 AC AAU68769;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Human Wilms' tumour protein, WT1, antigenic peptide #164.
 XX
 KW Human; Wilms' tumour; WT1; pleural mesothelioma; antigen;
 KW leukaemia; acute myeloid leukaemia; ALL; chronic myeloid leukaemia; CML;
 KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;
 KW myeloproliferative syndrome; cancer; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200162920-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 22-FEB-2001; 2001WO-US05702.
 XX
 PR 22-FEB-2000; 2000US-184070P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Cheever MA, Gaiger A;
 XX
 DR WPI; 2001-648218/74.
 XX
 PT Composition for the treatment of mesothelioma comprises specific
 PT peptides i.e. Wilms' tumour antigen polypeptide derived antigenic
 PT fragments -
 XX
 PS Claim 1; Page 176; 242pp; English.
 XX
 CC The invention relates to the use of a composition comprising at least a
 CC first isolated peptide, of between 9 and 40 amino acids or a first
 CC nucleic acid, encoding the peptide, in the manufacture of a medicament
 CC for treating or preventing mesothelioma. The peptides are antigenic
 CC peptides derived from the Wilms' tumour protein WT1. The composition is
 CC useful for the treatment of mesothelioma, Wilms' tumour, preferably
 CC pleural mesothelioma and other WT1 associated malignancies e.g.
 CC leukaemia (including acute myeloid leukaemia, ALL, chronic myeloid
 CC leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL),
 CC myelodysplastic syndromes, myeloproliferative syndromes and cancers
 CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,
 CC preferably humans. The present sequence is an antigenic peptide of
 CC the invention derived from human WT1.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 1 RMPFNAPYL 9

RESULT 6
 AAU68877
 ID AAU68877 standard; Peptide; 9 AA.

AC AAU68877;
 DT 16-JAN-2002 (first entry)

DE Mouse Wilm's tumour protein, WT1, antigenic peptide #46.

XX Mouse; Wilms' tumour; WT1; pleural mesothelioma; antigen;
 KW Leukaemia; acute myeloid leukaemia; AML; chronic myeloid leukaemia; CML;
 KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;
 KW myeloproliferative syndrome; cancer; cyclostatic.

OS Mus musculus.
 XX WO200162920-A2.

XX 30-AUG-2001.

XX 22-FEB-2001; 2001WO-US05702.

XX 22-FEB-2000; 2000US-184070P.

XX (CORI-) CORIXA CORP.

PI Cheever MA, Gajger A;

XX WPI; 2001-648218/74.

PT Composition for the treatment of mesothelioma comprises specific
 PT peptides i.e. Wilms' tumour antigen polypeptide derived antigenic
 PT fragments -

XX Claim 1; Page 24; 242pp; English.

PS The invention relates to the use of a composition comprising at least a
 PS first isolated peptide, of between 9 and 40 amino acids or a first
 PS nucleic acid, encoding the peptide, in the manufacture of a medicament
 PS for treating or preventing mesothelioma. The peptides are antigenic
 PS peptides derived from the Wilms' tumour protein WT1. The composition is
 PS useful for the treatment of mesothelioma, Wilms' tumour, preferably
 PS pleural mesothelioma and other WT1 associated malignancies e.g.
 CC leukaemia (including acute myeloid leukaemia, AML, chronic myeloid
 CC leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL),
 CC myelodysplastic syndromes, myeloproliferative syndromes and cancers
 CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,
 CC preferably humans. The present sequence is an antigenic peptide of
 CC the invention derived from mouse WT1.

XX Sequence 9 AA;

Query Match 100.0%; Score 51; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 1 RMPFNAPYL 9

RESULT 7

AA62002
 ID AA62002 standard; Peptide; 9 AA.

AC AA62002;

DT 06-JUL-2001 (first entry)

DE Human WT1 immunogenic peptide SEQ ID NO: 185.

XX Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;
 KW chromosome 11p13; zinc finger transcription factor.

OS Homo sapiens.

XX WO200125273-A2.

XX 12-APR-2001.

XX 04-OCT-2000; 2000WO-US27465.

XX 04-OCT-1999; 99US-0157459.

XX (CORI-) CORIXA CORP.

PI Skeiky YAW, Xu J, Cheever MA, Reed SG;

XX WPI; 2001-328324/34.

PT Polypeptide comprising part of the Wilm's Tumour gene product sequence is
 PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
 PT and cancer associated with WT1 -

XX Claim 4; Page 183; 228pp; English.

PS The present invention describes compositions comprising peptides derived
 PS from the Wilm's tumour protein WT1 and methods for their use in treating
 PS malignant diseases. Peptides derived from both the murine and human WT1
 PS proteins are provided. The human WT1 gene is found on chromosome 11p13,
 PS and the protein was shown to be a zinc finger transcription factor. The
 PS immunogenic peptides of the invention are particularly useful in the
 PS diagnosis and treatment of cancer and leukaemia. The present sequence is
 PS a polypeptide described in the exemplification of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 51; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 1 RMPFNAPYL 9

RESULT 8

AA62110
 ID AA62110 standard; Peptide; 9 AA.

AC AA62110;

DT 06-JUL-2001 (first entry)

DE Mouse WT1 immunogenic peptide SEQ ID NO: 293.

XX Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;
 KW chromosome 11p13; zinc finger transcription factor.

OS Mus musculus.

XX WO200125273-A2.

XX 12-APR-2001.

PF 04-OCT-2000; 2000WO-US27465.
 XX 04-OCT-1999; 99US-0157459.
 XX (CORI-) CORIXA CORP.
 PA Skelky YAW, Xu J, Cheever MA, Reed SG;
 PI WPI: 2001-328324/34.
 XX
 DR Polypeptide comprising part of the Wilm's Tumour gene product sequence is
 XX used in the diagnosis and treatment of malignant diseases e.g. leukemia
 PT and cancer associated with WT1 -
 XX Claim 4; Page 200; 228pp; English.
 PS
 XX The present invention describes compositions comprising peptides derived
 CC from the Wilm's tumour protein WTI and methods for their use in treating
 CC malignant diseases. Peptides derived from both the murine and human WTI
 CC proteins are provided. The human WTI gene is found on chromosome 11p13,
 CC and the protein was shown to be a zinc finger transcription factor. The
 CC immunogenic peptides of the invention are particularly useful in the
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is
 CC a polypeptide described in the exemplification of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 1 RMPFNAPYL 9

RESULT 9
 ABG79100
 ID ABG79100 standard; Peptide: 9 AA.
 XX
 AC ABG79100;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human WT1 class I HLA widely expressed antigen peptide #1.
 XX
 KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
 KW Lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
 KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
 KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
 KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
 KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
 KW cytostatic; human.
 XX
 OS Homo sapiens.
 XX
 FN WO200264057-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 15-FEB-2002; 2002WO-US05212.
 XX
 FR 15-FEB-2001; 2001US-268687P.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Wang R;
 XX
 DR WPI: 2002-627577/67.
 XX
 PT Novel composition for treating a disease in an animal, comprises an
 PT immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody -

XX Disclosure; Page 19; 61pp; English.
 PS
 XX The invention relates to a composition (I) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (1) a vaccine comprising (I), CPP
 CC associated with an antigen, and a pharmaceutically acceptable carrier
 CC and (2) preparing a composition for a disease, by providing (I)
 CC and CPP associated with an antigen for disease, and introducing the
 CC antigen-associated CPP to (I), where antigen enters into the cell.
 CC The antigens are, for example, tumour antigen derived epitopes
 CC recognised by tumour infiltrating lymphocytes (TIL) of HLA (human
 CC leukocyte antigen) class I or II. The composition is useful for enhancing
 CC immunity in an animal to a disease, by administering a mature dendritic
 CC cell comprising CPP associated with an antigen to disease, to the animal,
 CC such that following the administration, animal is protected from disease,
 CC where the animal comprises both CD4+ and CD8+ T cells. It is also useful
 CC for treating a disease (e.g. cancer, tumour, melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, leukaemia,
 CC Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer,
 CC kidney cancer, adenocarcinoma, breast cancer, prostate cancer,
 CC ovarian cancer and pancreatic cancer). The animal is further subjected to
 CC a cancer treatment including surgery, radiation, chemotherapy or gene
 CC therapy. The administration of (I), preferably dendritic cell is prior
 CC to, subsequent to or concurrent with, the cancer treatment. The present
 CC sequence is a tumour antigen derived epitope for inclusion in the
 CC composition of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 1 RMPFNAPYL 9

RESULT 10
 ABG33239
 ID ABG33239 standard; Peptide: 9 AA.
 XX
 AC ABG33239;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human WT1 immunogenic peptide #162.
 XX
 KW Human; mouse; cytostatic; immunostimulant; WTI; cancer;
 KW immune response.
 KW
 KW Homo sapiens.
 XX
 OS
 XX
 FN WO200228414-A1.
 XX
 PD 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001WO-US31139.
 XX
 FR 06-OCT-2000; 2000US-0684361.
 XX
 FR 09-OCT-2000; 2000US-0685830.
 XX
 PR 15-FEB-2001; 2001US-0785019.
 XX
 PR 24-AUG-2001; 2001US-0938864.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI (GAIG/) GAIGER A.
 XX
 DR Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
 XX Sleath PR, Mosman S, Evans L, Spies AG, Boydston J;
 XX WPI: 2002-352217/38.
 XX

Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for treating and diagnosing cancer in a patient -

Example 4; Page 194; 260pp; English.

The invention relates to an isolated WT1 polynucleotide (I) and polypeptide encoded by (I). The WT1 polynucleotides and polypeptides are used for treating and detecting cancer in a patient, and for stimulating an immune response in patient. ABG33070-ABG33405 represent WT1 amino acid sequences of the invention.

Sequence 9 AA;

Query Match 100.0%; Score 51; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 1 RMPFNAPYL 9

RESULT 11
 ABG33347
 ID ABG33347 standard; Peptide; 9 AA.

AC ABG33347;
 DT 15-JUL-2002 (first entry)

DE Mouse WT1 immunogenic peptide #44.

KW Human; mouse; cytostatic; immunostimulant; WT1; cancer;
 KW Immune response.

OS Mus musculus.

PN WO200228414-A1.

PD 11-APR-2002.

PF 03-OCT-2001; 2001WO-US31139.

PR 06-OCT-2000; 2000US-0684361.

PR 09-OCT-2000; 2000US-0685830.

PR 15-FEB-2001; 2001US-0785019.

PR 24-AUG-2001; 2001US-0938864.

PA (CORI-) CORIXA CORP.

PA (GAIG/) GAIGER A.

PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
 PI Sleath PR, Mosman S, Evans L, Spies AG, Boydston J;

DR WPI: 2002-352217/38.

XX Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
 XX treating and diagnosing cancer in a patient -

XX Example 4; Page 210; 260pp; English.

XX The invention relates to an isolated WT1 polynucleotide (I) and
 XX polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
 XX are used for treating and detecting cancer in a patient, and for
 XX stimulating an immune response in patient. ABG33070-ABG33405
 XX represent WT1 amino acid sequences of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 51; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 1 RMPFNAPYL 9

RESULT 12

ID AAE17298 standard; peptide; 9 AA.

AC AAE17298;

DT 18-APR-2002 (first entry)

DE Human leukocyte antigen (HLA-A2.1) restricted peptide, DbI26.

KW Human; artificial antigen presenting cell; APC; beta2-microglobulin;
 KW human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW cytotoxic T lymphocyte; CTL; T cell-specific antigen; TCA; antitumour;
 KW immune response; cancer.

OS Homo sapiens.

PN WO200194944-A2.

PD 13-DEC-2001.

PF 01-JUN-2001; 2001WO-US17981.

PR 02-JUN-2000; 2000US-209157P.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PI Sadelain M, Latouche J;

DR WPI: 2002-139667/18.

XX Artificial antigen presenting cells for activating T lymphocytes,
 XX comprises eukaryotic cell expressing antigen presenting complex having
 XX beta2-microglobulin, exogenous accessory molecule, human leukocyte
 XX antigen molecule and protein -

XX Example 17; Page 40; 75pp; English.

XX The present invention relates to an artificial antigen presenting cell
 XX (APC) comprising a eukaryotic cell expressing an antigen presenting
 XX complex comprising beta2-microglobulin, an exogenous accessory molecule,
 XX a human leukocyte antigen (HLA) (major histocompatibility complex, MHC)
 XX molecule of a single type and a protein that is processed intracellularly
 XX to produce an exogenous T cell-specific epitope. The invention also
 XX relates to methods for activation of T lymphocytes. The method is also
 XX useful for identifying within a test population of cytotoxic T
 XX lymphocytes (CTLs), CTLs specifically activated against a known T-cell
 XX specific antigen (TCA), which is useful for diagnostic purposes. APC is
 XX also useful for activating CTLs, by contacting APC with a suitable
 XX population of T lymphocytes under conditions suitable for the activation
 XX and isolating the activated CTLs. APC is further useful for the
 XX investigation of primary T cell activation and diagnostic applications
 XX here primary T cell activation allow discovery of antigens and accessory
 XX molecules, and diagnostic applications include cell-based assays for
 XX quantifying immune response in normal, infected or treated (vaccinated)
 XX patients. Composition comprising APC or activated T cells produced by
 XX utilizing APC is useful for eliciting an antitumour response. The
 XX invention is used for the treatment of cancer. The present sequence is
 XX human HLA-A2.1 restricted peptide used in additional APC-induced CTL-
 XX activation.

XX Sequence 9 AA;

Query Match 100.0%; Score 51; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9

Db 1 RMPFNAPYL 9

RESULT 13
AAV98502 standard; Peptide; 23 AA.

31-JUL-2000 (first entry)
Human WT1 peptide SEQ ID NO:2.

WT1; immunotherapy; immunogenic; malignant disease; cancer; leukemia; metastatic disease; mouse; human; Wilm's tumour; immune response; vaccine.

Homo sapiens.

MO200018795-A2.

06-APR-2000.

30-SEP-1999; 99WO-US22819.

30-SEP-1998; 98US-0164223.

25-MAR-1999; 99US-0276484.

(CORI-) CORIXA CORP.

(GAIG/) GAIGER A.

Gaiger A, Cheever M;

WPI; 2000-293107/25.

Novel polypeptides comprising an immunogenic portion of a native WT1 polypeptide, useful for inhibiting the development of malignant diseases associated with WT1 expression e.g. leukemia or cancer

Claim 4; Page 46; 193pp; English.

The present invention describes polypeptides (I) comprising an immunogenic portion of a native Wilm's Tumour gene product polypeptide, WT1, (or variants of the immunogenic portion retaining the ability to react with WT1-specific antisera and/or T-cell lines or clones) and comprising 16 consecutive amino acids (aa) or less of a native WT1 polypeptide. The polypeptides are useful therapeutically and to manufacture medicaments for enhancing/inducing an immune response in patients. The polypeptides, mimetics or polynucleotides can be included with a carrier/excipient in pharmaceutical compositions or with a non-specific immune response enhancer (e.g. an adjuvant or enhancer preferentially enhancing a T cell response) in vaccines. Pharmaceutical compositions and vaccines can be administered to human patients to enhance or induce an immune response specific for WT1 or a cell expressing WT1, useful to inhibit the development of malignant diseases associated with WT1 expression, e.g. leukemia (especially acute/chronic myeloid leukemia or acute lymphocytic leukemia) or cancer (especially breast, lung, thyroid or gastrointestinal cancer, or a melanoma). AAV98501 to AAV98811 represent polypeptide sequences, and AAA13848 to AAA13862 represent PCR primers, used in the exemplification of the present invention.

Sequence 23 AA;

Query Match 100.0%; Score 51; DB 21; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RMPFNAPYL 9
10 RMPFNAPYL 18

RESULT 14
AAV98503 standard; Peptide; 23 AA.

31-JUL-2000 (first entry)
Mouse WT1 peptide SEQ ID NO:3.

WT1; immunotherapy; immunogenic; malignant disease; cancer; leukemia; metastatic disease; mouse; human; Wilm's tumour; immune response; vaccine.

Mus musculus.

MO200018795-A2.

06-APR-2000.

30-SEP-1999; 99WO-US22819.

30-SEP-1998; 98US-0164223.

25-MAR-1999; 99US-0276484.

(CORI-) CORIXA CORP.

(GAIG/) GAIGER A.

Gaiger A, Cheever M;

WPI; 2000-293107/25.

Novel polypeptides comprising an immunogenic portion of a native WT1 polypeptide, useful for inhibiting the development of malignant diseases associated with WT1 expression e.g. leukemia or cancer

Example 3; Page 46; 193pp; English.

The present invention describes polypeptides (I) comprising an immunogenic portion of a native Wilm's Tumour gene product polypeptide, WT1, (or variants of the immunogenic portion retaining the ability to react with WT1-specific antisera and/or T-cell lines or clones) and comprising 16 consecutive amino acids (aa) or less of a native WT1 polypeptide. The polypeptides are useful therapeutically and to manufacture medicaments for enhancing/inducing an immune response in patients. The polypeptides, mimetics or polynucleotides can be included with a carrier/excipient in pharmaceutical compositions or with a non-specific immune response enhancer (e.g. an adjuvant or enhancer preferentially enhancing a T cell response) in vaccines. Pharmaceutical compositions and vaccines can be administered to human patients to enhance or induce an immune response specific for WT1 or a cell expressing WT1, useful to inhibit the development of malignant diseases associated with WT1 expression, e.g. leukemia (especially acute/chronic myeloid leukemia or acute lymphocytic leukemia) or cancer (especially breast, lung, thyroid or gastrointestinal cancer, or a melanoma). AAV98501 to AAV98811 represent polypeptide sequences, and AAA13848 to AAA13862 represent PCR primers, used in the exemplification of the present invention.

Sequence 23 AA;

Query Match 100.0%; Score 51; DB 21; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RMPFNAPYL 9
10 RMPFNAPYL 18

RESULT 15
AAU68601

ID AAU68601 standard; Peptide: 23 AA.
 AC AAU68601;
 DT 16-JAN-2002 (first entry)
 DE Human Wilm's tumour proteoln, WT1, antigenic peptide #2.
 KM Human; Wilms' tumour; WT1; pleural mesothelioma; antigen;
 KW leukaemia; acute myeloid leukaemia; AML; chronic myeloid leukaemia; CML;
 KM acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;
 KW myeloproliferative syndrome; cancer; cytostatic.
 OS Homo sapiens.
 PN WO200162920-A2.
 PD 30-AUG-2001.
 PP 22-FEB-2001; 2001WO-US05702.
 PR 22-FEB-2000; 2000US-184070P.
 PS (CORI-) CORIXA CORP.
 PI Cheever MA, Galger A;
 XX WPI; 2001-648218/74.
 DR WPI; 2001-648218/74.
 PT Composition for the treatment of mesothelioma comprises specific
 PR peptides i.e. Wilms' tumour antigen polypeptide derived antigenic
 PT fragments -
 XX Claim 1; Page 24; 242pp; English.
 XX The invention relates to the use of a composition comprising at least a
 CC first isolated peptide, of between 9 and 40 amino acids or a first
 CC nucleic acid, encoding the peptide, in the manufacture of a medicament
 CC for treating or preventing mesothelioma. The peptides are antigenic
 CC peptides derived from the Wilms' tumour protein WT1. The composition is
 CC useful for the treatment of mesothelioma, Wilms' tumour, preferably
 CC pleural mesothelioma and other WT1 associated malignancies e.g.
 CC leukaemia (including acute myeloid leukaemia, ALL, chronic myeloid
 CC leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL),
 CC myelodysplastic syndromes, myeloproliferative syndromes and cancers
 CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,
 CC preferably humans. The present sequence is an antigenic peptide of
 CC the invention derived from human WT1.
 SO Sequence 23 AA;
 QY Query Match 100.0%; Score 51; DB 22; Length 23;
 AC Best Local Similarity 100.0%; Pred. No. 0.007;
 AC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DT 1 RMPFNAPYL 9
 DB 10 RMPFNAPYL 18
 RESULT 16
 ID AAU68602 standard; Peptide: 23 AA.
 AC AAU68602;
 DT 16-JAN-2002 (first entry)
 DE Mouse Wilm's tumour protein, WT1, antigenic peptide #1.
 KM Mouse; Wilms' tumour; WT1; pleural mesothelioma; antigen;
 KW leukaemia; acute myeloid leukaemia; AML; chronic myeloid leukaemia; CML;
 KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;

KM myeloproliferative syndrome; cancer; cytostatic.
 OS Mus musculus.
 PN WO200162920-A2.
 PD 30-AUG-2001.
 PP 22-FEB-2001; 2001WO-US05702.
 PR 22-FEB-2000; 2000US-184070P.
 PS (CORI-) CORIXA CORP.
 PI Cheever MA, Galger A;
 XX WPI; 2001-648218/74.
 DR WPI; 2001-648218/74.
 PT Composition for the treatment of mesothelioma comprises specific
 PR peptides i.e. Wilms' tumour antigen polypeptide derived antigenic
 PT fragments -
 XX Claim 1; Page 24; 242pp; English.
 XX The invention relates to the use of a composition comprising at least a
 CC first isolated peptide, of between 9 and 40 amino acids or a first
 CC nucleic acid, encoding the peptide, in the manufacture of a medicament
 CC for treating or preventing mesothelioma. The peptides are antigenic
 CC peptides derived from the Wilms' tumour protein WT1. The composition is
 CC useful for the treatment of mesothelioma, Wilms' tumour, preferably
 CC pleural mesothelioma and other WT1 associated malignancies e.g.
 CC leukaemia (including acute myeloid leukaemia, ALL, chronic myeloid
 CC leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL),
 CC myelodysplastic syndromes, myeloproliferative syndromes and cancers
 CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,
 CC preferably humans. The present sequence is an antigenic peptide of
 CC the invention derived from mouse WT1.
 SO Sequence 23 AA;
 QY Query Match 100.0%; Score 51; DB 22; Length 23;
 AC Best Local Similarity 100.0%; Pred. No. 0.007;
 AC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DT 1 RMPFNAPYL 9
 DB 10 RMPFNAPYL 18
 RESULT 17
 ID AAG61834 standard; Peptide: 23 AA.
 AC AAG61834;
 DT 06-JUL-2001 (first entry)
 DE Human WT1 immunogenic peptide SEQ ID NO: 2.
 KM Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;
 KW chromosome 11p13; zinc finger transcription factor.
 OS Homo sapiens.
 PN WO200125273-A2.
 PD 12-APR-2001.
 PP 04-OCT-2000; 2000WO-US27465.
 PR 04-OCT-1999; 99US-0157459.
 PS (CORI-) CORIXA CORP.

XX Skeiky YAW, Xu J, Cheever MA, Reed SG;
 PI WPI: 2001-328324/34.
 DR Polypeptide comprising part of the Wilm's Tumour gene product sequence is
 XX used in the diagnosis and treatment of malignant diseases e.g. leukemia
 PT and cancer associated with WT1 -
 XX Claim 4; Page 155; 228pp; English.
 PS The present invention describes compositions comprising peptides derived
 CC from the Wilm's tumour protein WT1 and methods for their use in treating
 CC malignant diseases. Peptides derived from both the murine and human WT1
 CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
 CC and the protein was shown to be a zinc finger transcription factor. The
 CC immunogenic peptides of the invention are particularly useful in the
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is
 CC a polypeptide described in the exemplification of the invention.
 SO Sequence 23 AA;
 SO Query Match 100.0%; Score 51; DB 22; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.007;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RMPFNAPYL 9
 |||||
 |||||
 DB 10 RMPFNAPYL 18
 RESULT 18
 AAG61835
 ID AAG61835 standard; Peptide: 23 AA.
 XX AAG61835;
 AC AAG61835;
 XX 06-JUL-2001 (first entry)
 DT Mouse WT1 immunogenic peptide SEQ ID NO: 3.
 XX Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;
 KW chromosome 11p13; zinc finger transcription factor.
 XX Mus musculus.
 OS WO200125273-A2.
 PN 12-APR-2001.
 PD 04-OCT-2000; 2000WO-US27465.
 PF 04-OCT-1999; 99US-0157459.
 PR (CORI-) CORIXA CORP.
 PA Skeiky YAW, Xu J, Cheever MA, Reed SG;
 PI WPI: 2001-328324/34.
 DR Polypeptide comprising part of the Wilm's Tumour gene product sequence is
 XX used in the diagnosis and treatment of malignant diseases e.g. leukemia
 PT and cancer associated with WT1 -
 XX Example 3; Page 155; 228pp; English.
 PS The present invention describes compositions comprising peptides derived
 CC from the Wilm's tumour protein WT1 and methods for their use in treating
 CC malignant diseases. Peptides derived from both the murine and human WT1
 CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
 CC and the protein was shown to be a zinc finger transcription factor. The
 CC immunogenic peptides of the invention are particularly useful in the
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is

CC a polypeptide described in the exemplification of the invention.
 XX Sequence 23 AA;
 SO Query Match 100.0%; Score 51; DB 22; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.007;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RMPFNAPYL 9
 |||||
 |||||
 DB 10 RMPFNAPYL 18
 RESULT 19
 ABG33071
 ID ABG33071 standard; Peptide: 23 AA.
 XX ABG33071;
 AC ABG33071;
 XX 15-JUL-2002 (first entry)
 DT Human WT1 immunogenic peptide #2.
 DE Human; mouse; cytostatic; immunostimulant; WT1; cancer;
 XX immune response.
 KW Homo sapiens.
 XX WO200228414-A1.
 PN 11-APR-2002.
 PD 03-OCT-2001; 2001WO-US31139.
 PF 06-OCT-2000; 2000US-0684361.
 PR 09-OCT-2000; 2000US-0685830.
 PR 15-FEB-2001; 2001US-0785019.
 PR 24-AUG-2001; 2001US-0938864.
 XX (CORI-) CORIXA CORP.
 PA (GAIQ/) GAIQER A.
 PI Gaiqer A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
 PI Sleath PR, Moseman S, Evans L, Spies AG, Boydston J;
 PI WPI: 2002-352217/38.
 DR Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
 XX treating and diagnosing cancer in a patient -
 XX Example 3; Page 155; 260pp; English.
 PS The invention relates to an isolated WT1 polynucleotide (1) and
 CC polypeptide encoded by (1). The WT1 polynucleotides and polypeptides
 CC are used for treating and detecting cancer in a patient, and for
 CC stimulating an immune response in patient. ABG33070-ABG33405
 CC represent WT1 amino acid sequences of the invention.
 XX Sequence 23 AA;
 SO Query Match 100.0%; Score 51; DB 23; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.007;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RMPFNAPYL 9
 |||||
 |||||
 DB 10 RMPFNAPYL 18
 RESULT 20
 ABG33072
 ID ABG33072 standard; Peptide: 23 AA.
 XX

AC ABG33072;
 XX 15-JUL-2002 (first entry)
 DT
 XX
 DE Mouse WT1 immunogenic peptide #1.
 XX
 KM Human; mouse; cytostatic; immunostimulant; WT1; cancer;
 KM Immune response.
 XX
 OS Mus musculus.
 XX
 EN W0200228414-A1.
 XX
 PD 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001WO-US31139.
 XX
 PR 06-OCT-2000; 2000US-0684361.
 PR 09-OCT-2000; 2000US-0685830.
 PR 15-FEB-2001; 2001US-0785019.
 PR 24-AUG-2001; 2001US-0938864.
 XX
 XX (CORI-) CORIXA CORP.
 PA (GAIG/) GAIGER A.
 XX
 PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
 PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
 DR WPI; 2002-352217/38.
 XX
 PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
 PT treating and diagnosing cancer in a patient -
 XX
 PS Example 3; Page 165; 260pp; English.
 XX
 CC The invention relates to an isolated WT1 polynucleotide (I) and
 CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
 CC are used for treating and detecting cancer in a patient, and for
 CC stimulating an immune response in patient. ABG33070-ABG33405
 CC represent WT1 amino acid sequences of the invention.
 XX
 SQ Sequence 23 AA;

PR 06-OCT-2000; 2000US-0684361.
 PR 09-OCT-2000; 2000US-0685830.
 PR 15-FEB-2001; 2001US-0785019.
 PR 24-AUG-2001; 2001US-0938864.
 XX
 XX (CORI-) CORIXA CORP.
 PA (GAIG/) GAIGER A.
 XX
 PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
 PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
 DR WPI; 2002-352217/38.
 DR N-PSDB; ABK69669.
 XX
 PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
 PT treating and diagnosing cancer in a patient -
 XX
 PS Claim 2; Page 226-227; 260pp; English.
 XX
 CC The invention relates to an isolated WT1 polynucleotide (I) and
 CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
 CC are used for treating and detecting cancer in a patient, and for
 CC stimulating an immune response in patient. ABG33070-ABG33405
 CC represent WT1 amino acid sequences of the invention.
 XX
 SQ Sequence 152 AA;

Query Match 100.0%; Score 51; DB 23; Length 152;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMPFNAPYL 9
 |||||
 DB 51 RMPFNAPYL 59

RESULT 22
 AAW47175
 ID AAW47175 standard; Protein: 154 AA.
 AC AAW47175;
 XX
 DT 01-JUN-1998 (first entry)
 XX
 DE Wilms' tumour polypeptide (WT33) proline and glutamine rich region.
 XX
 KW Wilms' tumour; WT33; cancer treatment; antibody production; WAGR;
 KW Denys-drash syndrome; WT1.
 XX
 OS Homo sapiens.
 XX
 EN US5726288-A.
 XX
 PD 10-MAR-1998.
 XX
 PF 02-AUG-1993; 93US-0102942.
 XX
 PR 02-AUG-1993; 93US-0102942.
 PR 13-NOV-1989; 89US-0435780.
 PR 13-NOV-1990; 90US-0614161.
 XX
 PA (MASI) MASSACHUSETTS INSTR TECHNOLOGY.
 XX
 PI Bruening W, Buckler AJ, Call KM, Darveau A, Glaeser TM;
 PI Haber DA, Housman DE, Ico CY, Pelletier J, Rose EA;
 DR WPI; 1998-192828/17.
 XX
 PT New Wilms' tumour polypeptide - useful for, e.g. cancer treatment
 PT and antibody production
 XX
 PS Claim 2; Fig 4; 42pp; English.
 XX

CC This sequence represents the proline and glutamine rich region of a new
 CC Wilms' tumour (WT33) polypeptide. The Wilms' tumour gene (WT1) is
 CC associated with 11p3 locus on the human chromosome. This proline and
 CC glutamine rich region indicates that the Wilms' tumour polypeptide has
 CC a role in transcription regulation. The polypeptide or immunogenic
 CC fragments of the polypeptide can be used to treat cancerous or
 CC precancerous conditions (especially Wilms' tumour), or to raise
 CC antibodies for diagnostic use. The product allow detection of risk of
 CC development of Wilms' tumour, e.g. in diseases such as WAGR and
 CC Denys-Drash syndrome, to be assessed prior to current methods of
 CC detection.

SO Sequence 154 AA;

Query Match 100.0%; Score 51; DB 19; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 Db 40 RMPFNAPYL 48

RESULT 23

AG78445 standard; Protein; 154 AA.

AG78445;

12-APR-2002 (first entry)

Amino acid sequence of the proline/glutamine rich region of WT33.

Tumour; oncogene; retinoblastoma; chromosome 11p13; zinc finger;

Wilms' tumour disease; WT33; human.

Homo sapiens.

US6316599-B1.

13-NOV-2001.

09-MAR-1998; 98US-0037179.

02-AUG-1993; 93US-0102942.

13-NOV-1989; 89US-0435780.

13-NOV-1990; 90US-0614161.

(MASI) MASSACHUSETTS INST TECHNOLOGY.

Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;

Rose EA, Housman DE, Breuning W, Darveau A;

WPI; 2002-074379/10.

Antibodies specific for Wilms' tumour (WT) protein variant WT33, useful

in immunoassays to detect WT33 in samples and diagnose e.g. Sporadic

Wilms' tumours

Claim 5; Fig 4; 45pp; English.

This invention relates to an isolated antibody specific for a protein

encoded by a Wilms' tumour DNA. The antibodies may be used in

immunoassays to detect the presence of the Wilms' tumour variant WT33 in

biological samples. They may be used in this way to diagnose sporadic

Wilms' tumours, as seen in Wilms' tumour. The antibody makes it possible

to detect proteins encoded by DNA which is clearly derived from the 11p13

Wilms' tumour gene. This is particularly valuable because the treatment

of Wilms' tumour represents one of the clearest examples of success in

paediatric oncology. As a result of the development of effective

therapeutic regimens. A diagnostic test would allow early detection of

the disease. The presence of the disease can be confirmed, thus making

it possible to intervene therapeutically prior to or at an earlier

CC stage in the development of the disease. This sequence represents
 CC the proline/glutamine rich region of the WT33 Wilms' tumour protein,
 CC encoded by the gene located on chromosome 11p13.

SO Sequence 154 AA;

Query Match 100.0%; Score 51; DB 23; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 Db 40 RMPFNAPYL 48

RESULT 24

ABG71422 standard; Protein; 154 AA.

ABG71422;

10-FEB-2003 (first entry)

Human Wilms' tumour gene WT33 polypeptide proline/glutamine rich region.

Human; Wilms' tumour gene; WT33; cytostatic; Wilms' tumour; leukaemia;

testicular cancer; ovarian cancer; proline/glutamine rich region.

Homo sapiens.

US2002128196-A1.

12-SEP-2002.

12-NOV-2001; 2001US-0993215.

02-AUG-1993; 93US-0102942.

09-MAR-1998; 98US-0037179.

13-NOV-1989; 89US-0435780.

13-NOV-1990; 90US-0614161.

(MASI) MASSACHUSETTS INST TECHNOLOGY.

Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;

Rose EA, Housman DE, Breuning W, Darveau A;

WPI; 2003-066910/06.

Pharmaceutical composition for treating cancer or precancerous

condition such as Wilms' tumor, leukemia, testicular and ovarian cancer

associated with Wilms' tumour gene, and for inducing immune and antibody

responses

Claim 1; Fig 4; 41pp; English.

The invention relates to a pharmaceutical composition comprising a

polypeptide encoded by a Wilms' tumour gene. The composition is useful

for treating cancer or precancerous conditions (such as Wilms' tumour,

leukaemia, testicular and ovarian cancer) associated with the Wilms'

tumour gene in an individual, for inducing an immune response which

results in antibody production in a mammal, and for inducing an antibody

response by administering the composition to the mammal. This sequence

represents a human Wilms' tumour gene polypeptide WT33 proline/glutamine

rich region.

Sequence 154 AA;

Query Match 100.0%; Score 51; DB 24; Length 154;

Best Local Similarity 100.0%; Pred. No. 0.055;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9

DB 40 RMPFNAPYL 48

RESULT 25

AAR85066 standard; Protein; 210 AA.

02-FEB-1996 (first entry)

Wilms' tumour antigen WT1-6F.

Wilms' tumour; WT1-6F; monoclonal antibody; leukaemia.

Chimeric Homo sapiens;

Chimeric synthetic.

Key Location/Qualifiers

1..11 /Label= Histidine_fusion_peptide

/note= "hexa-histidine peptide used to facilitate fusion protein purification"

Protein 12..192 /label= WT1

Peptide 193..219 /note= "vector-derived amino acids"

MO9529995-A1.

09-NOV-1995.

25-APR-1995; 95WO-US05523.

28-APR-1994; 94US-0234783.

(WIST-) WISTAR INST ANATOMY & BIOLOGY.

Herlym M, Morris J, Rauscher FJ, Rodeck U;

WPI; 1995-393072/50.

N-PSDB; AAT02462.

Monoclonal antibodies specific for Wilms' tumour protein antigen WT1

- useful for detecting, monitoring and diagnosing malignancies

characterised by expression of WT1 protein, e.g. Leukaemia

Example 1; Page 37-38; 54pp; English.

Wilms' tumor antigen WT1-6F (AAR85066) is based on amino acids

1-181 of the native sequence, plus additional N- and C-terminal

sequences, and is encoded by synthetic DNA (AAT02462) optimized for

expression in E. coli. WT1-6F is used to raise monoclonal

antibodies specific for WT1.

Sequence 210 AA;

Query Match 100.0%; Score 51; DB 16; Length 210;

Best Local Similarity 100.0%; Pred. No. 0.077;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9

Db 137 RMPFNAPYL 145

RESULT 26

AAW22883

AAW22883 standard; Protein; 210 AA.

AAW22883;

25-MAR-2003 (updated)

DT 24-SEP-1997 (first entry)

Wilms' tumour protein antigen WT1-6F.

Wilms' tumour; WT1; antigen; WT1-6F; monoclonal; antibody;

diagnosis; mesothelioma; prostate; ovarian; cancer; leukaemia;

leukemia.

Homo sapiens.

Synthetic.

Key Location/Qualifiers

1..11 /note= "histidine fusion peptide to facilitate

purification"

Protein 12..192 /note= "amino acids 1-181 of WT1 protein"

Region 193..219 /note= "vector sequences added during cloning"

US633142-A.

27-MAY-1997.

01-JUN-1995; 95US-0456907.

01-JUN-1995; 95US-0456907.

28-APR-1994; 94US-0234783.

(WIST-) WISTAR INST ANATOMY & BIOLOGY.

Herlym M, Morris J, Rauscher FJ, Rodeck U;

WPI; 1997-297358/27.

N-PSDB; AAT75529.

Diagnosis of mesothelioma and monitoring of leukaemia therapy -

using monoclonal antibodies against Wilms' tumour 1 antigen

Example 1; Columns 17-20; 21pp; English.

The present sequence is the Wilms' tumour protein antigen

WT1-6F, which comprises amino acids 1-181 of the Wilms' tumour 1

antigen (WT1) protein. WT1-6F can be used to raise monoclonal

antibodies (MAB), e.g. H2, H7 and/or H17, which are secreted by

the hybridoma cell lines ATCC 11598, 11599 and 11600. The MAB can

be used to diagnose mesothelioma, prostate cancer, ovarian cancer

or leukaemia by binding an antigen in a whole blood, serum, plasma,

synovial fluid or tissue sample, or monitor therapy in leukaemia

patients by binding an antigen in a whole blood, plasma, serum,

urine or bone marrow sample, indicating the presence of active

leukaemia cells. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 210 AA;

Query Match 100.0%; Score 51; DB 18; Length 210;

Best Local Similarity 100.0%; Pred. No. 0.077;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9

Db 137 RMPFNAPYL 145

RESULT 27

ABG33395

ABG33395 standard; Protein; 214 AA.

ABG33395;

15-JUL-2002 (first entry)

XX AC ABG71420;
 XX DT 10-FEB-2003 (first entry)
 XX DE Human WILMS' tumour gene WT33 polypeptide.
 XX KM Human; Wilms' tumour gene; WT33; cytostatic; Wilms' tumour; leukaemia;
 XX KM testicular cancer; ovarian cancer.
 XX OS Homo sapiens.
 XX PN US2002128196-A1.
 XX PD 12-SEP-2002.
 XX PE 12-NOV-2001; 2001US-0993215.
 XX PR 02-AUG-1993; 93US-0102942.
 XX PR 09-MAR-1998; 98US-0037172.
 XX PR 13-NOV-1989; 89US-0435780.
 XX PR 13-NOV-1990; 90US-0614161.
 XX PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX PI Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;
 XX PI Rose EA, Housman DE, Brunning W, Darveau A;
 XX DR WPI; 2003-066910/06.
 XX DR N-PSDB; ABS57419.
 XX PT Pharmaceutical composition for treating cancer or precancerous
 XX PT condition such as Wilms' tumor, leukemia, testicular and ovarian cancer
 XX PT associated with Wilms' tumor gene, and for inducing immune and antibody
 XX PT responses
 XX PS Example 1; Fig 3; 41pp; English.
 XX CC The invention relates to a pharmaceutical composition comprising a
 XX CC polypeptide encoded by a Wilms' tumour gene. The composition is useful
 XX CC for treating cancer or precancerous conditions (such as Wilms' tumour,
 XX CC leukaemia, testicular and ovarian cancer) associated with the Wilms'
 XX CC tumour gene in an individual, for inducing an immune response which
 XX CC results in antibody production in a mammal, and for inducing an antibody
 XX CC response by administering the composition to the mammal. This sequence
 XX CC represents a human Wilms' tumour gene polypeptide, WT33.
 XX CC
 XX CC Sequence 345 AA;
 XX SQ
 XX
 XX Query Match 100.0%; Score 51; DB 24; Length 345;
 XX Best Local Similarity 100.0%; Pred. No. 0.13; 0; Indels 0; Gaps 0;
 XX Matches 9; Conservative 0; Mismatches 0;
 XX
 XX Oy 1 RMPFNAPYLL 9
 XX ||||||||
 XX ||||||||
 XX 42 RMPFNAPYLL 50
 XX DB
 XX
 XX RESULT 35
 XX ABG33394
 XX ID ABG33394 standard; Protein; 362 AA.
 XX AC ABG33394;
 XX DT 15-JUL-2002 (first entry)
 XX DE Human WT1-C.
 XX KM Human; mouse; cytostatic; immunostimulant; WT1; cancer;
 XX KM immune response.
 XX OS Homo sapiens.
 XX PI

PN W0200228414-A1.
 XX PD 11-APR-2002.
 XX PE 03-OCT-2001; 2001WO-US311139.
 XX PR 06-OCT-2000; 2000US-0684361.
 XX PR 09-OCT-2000; 2000US-0685830.
 XX PR 15-FEB-2001; 2001US-0785019.
 XX PR 24-AUG-2001; 2001US-0938864.
 XX PA (CORI-) CORIXA CORP.
 XX PA (GAI G/) GAIGER A.
 XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
 XX PI Sleath PR, Moseman S, Evans L, Spies AG, Boydston J;
 XX DR WPI; 2002-352217/38.
 XX DR N-PSDB; ABK69683.
 XX PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
 XX PT treating and diagnosing cancer in a patient
 XX PS Claim 2; Page 246-248; 260pp; English.
 XX CC The invention relates to an isolated WT1 polynucleotide (I) and
 XX CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
 XX CC are used for treating and detecting cancer in a patient, and for
 XX CC stimulating an immune response in patient. ABG33070-ABG33405
 XX CC represent WT1 amino acid sequences of the invention.
 XX CC
 XX CC Sequence 362 AA;
 XX SQ
 XX
 XX Query Match 100.0%; Score 51; DB 23; Length 362;
 XX Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
 XX Matches 9; Conservative 0; Mismatches 0;
 XX
 XX Oy 1 RMPFNAPYLL 9
 XX ||||||||
 XX ||||||||
 XX 59 RMPFNAPYLL 67
 XX DB
 XX
 XX RESULT 36
 XX ABG33390
 XX ID ABG33390 standard; Protein; 369 AA.
 XX AC ABG33390;
 XX DT 15-JUL-2002 (first entry)
 XX DE Human WT1-C.
 XX KM Human; mouse; cytostatic; immunostimulant; WT1; cancer;
 XX KM immune response.
 XX OS Homo sapiens.
 XX PN W0200228414-A1.
 XX PD 11-APR-2002.
 XX PE 03-OCT-2001; 2001WO-US311139.
 XX PR 06-OCT-2000; 2000US-0684361.
 XX PR 09-OCT-2000; 2000US-0685830.
 XX PR 15-FEB-2001; 2001US-0785019.
 XX PR 24-AUG-2001; 2001US-0938864.
 XX PA (CORI-) CORIXA CORP.
 XX PA (GAI G/) GAIGER A.
 XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
 XX PI Sleath PR, Moseman S, Evans L, Spies AG, Boydston J;

XX DR WPI: 2000-195264/17.
 XX PT Cancer antigens based on Wilm's tumor suppressor gene WT1 product or
 PT peptide derivatives, for cancer vaccines in treating leukemia and solid
 PT tumors e.g. stomach cancer, skin cancer, lung cancer and breast cancer
 XX PS Claim 2; Page 40-42; 48pp; Japanese.
 CC CC The present invention describes a cancer antigen containing the active
 CC component of Wilm's tumor suppressor gene WT1 product, or partial
 CC peptides, for cancer vaccines in treating leukemia and solid tumours.
 CC The cancer antigens are useful for cancer vaccines in treating
 CC leukaemia, bone-marrow abnormal formation syndrome, malignant lymphoma,
 CC multiple myeloma, stomach cancer, cancer of the large intestine, lung
 CC cancer, breast cancer, blastoma, liver cancer, skin cancer, bladder
 CC cancer, prostate cancer, uterus cancer, cervical cancer, or ovary
 CC cancer. The present sequence represents the human Wilm's tumour
 CC suppressor gene WT1 product.
 CC XX Sequence 449 AA;
 SO Query Match 100.0%; Score 51; DB 21; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RMPFNAPYL 9
 Db 126 RMPFNAPYL 134
 RESULT 47
 AAU68903
 ID AAU68903 standard; Protein; 449 AA.
 AC AAU68903;
 XX 16-JAN-2002 (first entry)
 DT Human Wilm's tumour protein, WT1.
 DE Human Wilm's tumour protein, WT1.
 XX Human; Wilm's tumour; WT1; pleural mesothelioma; antigen;
 KW leukaemia; acute myeloid leukaemia; ALL; chronic myeloid leukaemia; CML;
 KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;
 KM myeloproliferative syndrome; cancer; cytostatic.
 XX Homo sapiens.
 OS WO200162920-A2.
 PN 30-AUG-2001.
 PD 22-FEB-2001; 2001WO-US05702.
 PF 22-FEB-2000; 2000US-184070P.
 PR (CORI-) CORIXA CORP.
 XX (CORI-) CORIXA CORP.
 PA Cheever MA, Gaiger A;
 PI WPI: 2001-648218/74.
 DR Composition for the treatment of mesothelioma comprises specific
 XX peptides i.e. Wilm's tumour antigen polypeptide derived antigenic
 PT fragments -
 XX Disclosure; Page 250-251; 242pp; English.
 PS The invention relates to the use of a composition comprising at least a
 CC first isolated peptide, of between 9 and 40 amino acids or a first
 CC nucleic acid, encoding the peptide, in the manufacture of a medicament
 CC for treating or preventing mesothelioma. The peptides are antigenic
 CC peptides derived from the Wilm's tumour protein WT1. The composition is

CC useful for the treatment of mesothelioma, Wilm's tumour, preferably
 CC pleural mesothelioma and other WT1 associated malignancies e.g.
 CC leukaemia (including acute myeloid leukaemia, ALL, chronic myeloid
 CC leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL),
 CC myelodysplastic syndromes, myeloproliferative syndromes and cancers
 CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,
 CC preferably humans. The present sequence is the WT1 protein from which the
 CC antigenic peptides of the invention are derived.
 CC XX Sequence 449 AA;
 SO Query Match 100.0%; Score 51; DB 22; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RMPFNAPYL 9
 Db 126 RMPFNAPYL 134
 RESULT 48
 AAU68904
 ID AAU68904 standard; Protein; 449 AA.
 AC AAU68904;
 XX 16-JAN-2002 (first entry)
 DT Mouse Wilm's tumour protein, WT1.
 DE Mouse Wilm's tumour protein, WT1.
 XX Mouse; Wilm's tumour; WT1; pleural mesothelioma; antigen;
 KW leukaemia; acute myeloid leukaemia; ALL; chronic myeloid leukaemia; CML;
 KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;
 KM myeloproliferative syndrome; cancer; cytostatic.
 XX Mus musculus.
 OS WO200162920-A2.
 PN 30-AUG-2001.
 PD 22-FEB-2001; 2001WO-US05702.
 PF 22-FEB-2000; 2000US-184070P.
 PR (CORI-) CORIXA CORP.
 XX (CORI-) CORIXA CORP.
 PA Cheever MA, Gaiger A;
 PI WPI: 2001-648218/74.
 DR Composition for the treatment of mesothelioma comprises specific
 XX peptides i.e. Wilm's tumour antigen polypeptide derived antigenic
 PT fragments -
 XX Disclosure; Page 251-252; 242pp; English.
 PS The invention relates to the use of a composition comprising at least a
 CC first isolated peptide, of between 9 and 40 amino acids or a first
 CC nucleic acid, encoding the peptide, in the manufacture of a medicament
 CC for treating or preventing mesothelioma. The peptides are antigenic
 CC peptides derived from the Wilm's tumour protein WT1. The composition is
 CC useful for the treatment of mesothelioma, Wilm's tumour, preferably
 CC leukaemia (including acute myeloid leukaemia, ALL, chronic myeloid
 CC leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL),
 CC myelodysplastic syndromes, myeloproliferative syndromes and cancers
 CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,
 CC preferably humans. The present sequence is the WT1 protein from which the
 CC antigenic peptides of the invention are derived.
 CC XX Sequence 449 AA;
 SO


```

XX 02-AUG-1993; 93US-0102942.
PR 09-MAR-1998; 98US-0037179.
PR 13-NOV-1989; 89US-0435780.
PR 13-NOV-1990; 90US-0614161.
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PA Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA,
PI Rose EA, Housman DE, Bruening W, Darveau A;
XX WPI; 2002-690126/74.
DR N-PSDB; ABS53730.
XX
XX Treating cancer or precancerous condition associated with the Wilms'
PT tumour gene in individual, by administering polypeptide or polypeptide
PT encoded by Wilms' tumour DNA -
XX
XX Example 2; Fig 7; 41pp; English.
PS
XX The present invention relates to a new method of treating cancer or
CC precancerous condition associated with the Wilms' tumour gene. The method
CC of the invention is useful for treating a cancer or precancerous
CC condition associated with the Wilms' tumour gene in an individual, where
CC the cancer or precancerous condition is Wilms' tumour, leukemia,
CC testicular cancer or ovarian cancer. The present amino acid sequence
CC represents the mouse Wilms' tumour (WT) WTI protein that was used in the
CC methods of the invention.
XX
XX Sequence 449 AA;
SQ
Query Match 100.0%; Score 51; DB 23; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
|||
|||
|||
Db 126 RMPFNAPYL 134
RESULT 52
ABG33373
ID ABG33373 standard; Protein; 449 AA.
XX
XX ABG33373;
AC
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX Human WTI.
DE
XX
XX Human; mouse; cytostatic; immunostimulant; WTI; cancer;
KW
XX
XX Immune response.
OS
XX
XX Homo sapiens.
XX
XX WO200228414-A1.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-US31139.
XX
XX 06-OCT-2000; 2000US-0684361.
XX
XX 09-OCT-2000; 2000US-0685830.
XX
XX 15-FEB-2001; 2001US-0785019.
XX
XX 24-AUG-2001; 2001US-0938864.
XX
XX (CORI-) CORIXA CORP.
XX
XX (GAI/ ) GAIGER A.
XX
XX Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
XX
XX Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX
XX WPI; 2002-352217/38.

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XX Novel isolated WTI polynucleotide, and encoded polypeptide, useful for
PT treating and diagnosing cancer in a patient -
PT
XX Example 4; Figure 1; 260pp; English.
XX
XX The invention relates to an isolated WTI polynucleotide (I) and
CC polypeptide encoded by (I). The WTI polynucleotides and polypeptides
CC are used for treating and detecting cancer in a patient, and for
CC stimulating an immune response in patient. ABG33070-ABG33405
CC represent WTI amino acid sequences of the invention.
XX
XX Sequence 449 AA;
SQ
Query Match 100.0%; Score 51; DB 23; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
|||
|||
|||
Db 126 RMPFNAPYL 134
RESULT 53
ABG33374
ID ABG33374 standard; Protein; 449 AA.
XX
XX ABG33374;
AC
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX Mouse WTI.
DE
XX
XX Human; mouse; cytostatic; immunostimulant; WTI; cancer;
KW
XX
XX Immune response.
OS
XX
XX Mus musculus.
XX
XX WO200228414-A1.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-US31139.
XX
XX 06-OCT-2000; 2000US-0684361.
XX
XX 09-OCT-2000; 2000US-0685830.
XX
XX 15-FEB-2001; 2001US-0785019.
XX
XX 24-AUG-2001; 2001US-0938864.
XX
XX (CORI-) CORIXA CORP.
XX
XX (GAI/ ) GAIGER A.
XX
XX Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
XX
XX Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX
XX WPI; 2002-352217/38.
XX
XX Novel isolated WTI polynucleotide, and encoded polypeptide, useful for
PT treating and diagnosing cancer in a patient -
PT
XX Example 4; Figure 1; 260pp; English.
XX
XX The invention relates to an isolated WTI polynucleotide (I) and
CC polypeptide encoded by (I). The WTI polynucleotides and polypeptides
CC are used for treating and detecting cancer in a patient, and for
CC stimulating an immune response in patient. ABG33070-ABG33405
CC represent WTI amino acid sequences of the invention.
XX
XX Sequence 449 AA;
SQ
Query Match 100.0%; Score 51; DB 23; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 RMPFNAPYL 9
DB 126 RMPFNAPYL 134

RESULT 54
ABG33396
ID ABG33396 standard; Protein; 449 AA.

AC ABG33396;
DF 15-JUL-2002 (first entry)

DE Human WTI protein.
DE Human WTI protein.
DE Human; mouse; cyclostatic; immunostimulant; WTI; cancer;
KW immune response.

KM Homo sapiens.

OS W0200228414-A1.

PN 11-APR-2002.

PP 03-OCT-2001; 2001WO-US31139.

PR 06-OCT-2000; 2000US-0684361.

PR 09-OCT-2000; 2000US-0685830.

PR 15-FEB-2001; 2001US-0785019.

PR 24-AUG-2001; 2001US-0938864.

XX (CORI-) CORIXA CORP.

PA (GAI) GAIGER A.

PI Gager A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;

PI Sleeth PR, Mossman S, Evans U, Spies AG, Boydston J;

DR WPI; 2002-352217/38.

DR N-PSDB; ABK69676.

XX Novel isolated WTI polynucleotide, and encoded polypeptide, useful for

PT treating and diagnosing cancer in a patient -

PT Claim 2; Page 250-251; 260pp; English.

XX The invention relates to an isolated WTI polynucleotide (I) and

CC polypeptide encoded by (I). The WTI polynucleotides and polypeptides

CC are used for treating and detecting cancer in a patient, and for

CC stimulating an immune response in patient. ABG33070-ABG33405

CC represent WTI amino acid sequences of the invention.

CC Sequence 449 AA;

XX Query Match 100.0%; Score 51; DB 23; Length 449;

XX Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0;

XX Matches 9; Conservative 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
DB 126 RMPFNAPYL 134

RESULT 55
AAG78444
ID AAG78444 standard; Protein; 449 AA.

AC AAG78444;
DT 12-APR-2002 (first entry)

DE Murine WTI Wilm's tumour protein.

KM Tumour; oncogene; retinoblastoma; zinc finger;
KM Wilm's tumour disease; WTI; mouse.

XX Mus sp.

XX Key Location/Qualifiers
FT Domain 317-438
FT /label= zinc_finger_domains

XX US6316599-B1.

XX 13-NOV-2001.

XX 09-MAR-1998; 98US-0037179.

XX 02-AUG-1993; 93US-0102942.

XX 13-NOV-1989; 89US-0435780.

XX 13-NOV-1990; 90US-0614161.

XX (MASI) MASSACHUSETTS INSTR TECHNOLOGY.

XX Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;

XX Rose EA, Housman DE, Breunning W, Darveau A;

XX WPI; 2002-074379/10.

XX N-PSDB; AAH99946.

XX Example 4; Fig 9; 45pp; English.

XX This invention relates to an isolated antibody specific for a protein

XX encoded by a Wilm's tumour DNA. The antibodies may be used in

XX immunassays to detect the presence of the Wilm's tumour variant WT33 in

XX biological samples. They may be used in this way to diagnose sporadic

XX Wilm's tumours, as seen in Wilm's tumour. The antibody makes it possible

XX to detect proteins encoded by DNA which is clearly derived from the 11p13

XX Wilm's tumour gene. This is particularly valuable because the treatment

XX of Wilm's tumour represents one of the clearest examples of success in

XX paediatric oncology, as a result of the development of effective

XX therapeutic regimens. A diagnostic test would allow early detection of

XX the disease. The presence of the disease can be confirmed, thus making

XX it possible to intervene therapeutically prior to or at an earlier

XX stage in the development of the disease. This sequence represents

XX the WTI Wilm's tumour protein.

XX Sequence 449 AA;

XX Query Match 100.0%; Score 51; DB 23; Length 449;

XX Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0;

XX Matches 9; Conservative 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
DB 126 RMPFNAPYL 134

RESULT 56
AAG78446
ID AAG78446 standard; Protein; 449 AA.

AC AAG78446;
DT 12-APR-2002 (first entry)

DE Predicted WTI Wilm's tumour polypeptide of humans.

DE Tumour; oncogene; retinoblastoma; chromosome 11p13; zinc finger;
KW Wilm's tumour disease; WTI; human.
XX Homo sapiens.

PT associated with Wilms' tumor gene, and for inducing immune and antibody responses

PS Disclosure; Fig 8; 41pp; English.

CC The invention relates to a pharmaceutical composition comprising a polypeptide encoded by a Wilms' tumor gene. The composition is useful for treating cancer or precancerous conditions (such as Wilms' tumor, leukemia, testicular and ovarian cancer) associated with the Wilms' tumor gene in an individual, for inducing an immune response which results in antibody production in a mammal, and for inducing an antibody response by administering the composition to the mammal. This sequence represents a human Wilms' tumor gene polypeptide, WT1.

XX Sequence 449 AA;

Query Match 100.0%; Score 51; DB 24; Length 449;

Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9

DB 126 RMPFNAPYL 134

RESULT 59 ABB99880 standard; protein; 449 AA.

AC ABB99880;

DT 27-JAN-2003 (first entry)

DE Mouse Wilms' tumour antigen WT1.

Murine; murine; Wilms' tumour antigen; WT1; modified WT1 peptide; vaccine; immunotherapy; cancer; leukemia; solid tumour.

OS Mus sp.

Key Location/Qualifiers

FT Peptide 235..243 /note="Corresponds to SEQ ID NO:2 (ABB99881)"

FT WO200279253-A1.

PD 10-OCT-2002.

PF 22-MAR-2002; 2002WO-JP02794.

PR 22-MAR-2001; 2001JP-0083250.

PA (SUGI/) SUGIYAMA H.

PI Sugiyama H;

DR WPI; 2003-046799/04.

PT Cancer antigen WT1 modified peptides and DNA encoding them for cancer immunotherapy

PS Disclosure; Page 23-25; 30pp; Japanese.

CC The invention relates to modified peptides derived from the murine Wilms' tumor antigen WT1 (ABB99880). The peptides of the invention are 9-30 amino acids long and comprise the sequence Cys-Tyr-Thr-Trp-Asn-Gln-Met-Asn-Ieu (ABB99882). Cancer vaccines comprising modified WT1 peptides of the invention or DNA encoding them, and antigen presenting cells (including cytotoxic T-cells) which present a peptide of the invention (including with a major histocompatibility complex (MHC) class I molecule, can be used in the immunotherapy of leukemia and solid tumours such as cancers of the bladder, colon, breast, ovary, liver, skin, stomach, prostate, testis, lung and uterus. The present sequence represents

CC murine WT1.

XX Sequence 449 AA;

Query Match 100.0%; Score 51; DB 24; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9

DB 126 RMPFNAPYL 134

RESULT 60 ABB99880 standard; protein; 495 AA.

AC ABB99880;

DT 15-JUL-2002 (first entry)

DE Human WT1-LAMP fusion construct.

Human; mouse; cytotostatic; immunostimulant; WT1; cancer; immune response.

OS Homo sapiens.

Key Location/Qualifiers

FT Peptide 06..100 /note="Corresponds to SEQ ID NO:2 (ABB99881)"

FT WO200228414-A1.

PD 11-APR-2002.

PF 03-OCT-2001; 2001WO-US31139.

PR 06-OCT-2000; 2000US-0684361.

PR 09-OCT-2000; 2000US-0685830.

PR 15-FEB-2001; 2001US-0785019.

PR 24-AUG-2001; 2001US-0938864.

PA (CORI-) CORIXA CORP.

PI Galger A, McNeill PD, Smitgall M, Moulton G, Vedvick TS;

Sleath PR, Mosseman S, Evans L, Spies AG, Boydston J;

DR WPI; 2002-352217/38.

DR N-PSDB; ABR69678.

PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for treating and diagnosing cancer in a patient

PS Claim 2; Page 256-257; 260pp; English.

CC The invention relates to an isolated WT1 polynucleotide (I) and polypeptide encoded by (I). The WT1 polynucleotides and polypeptides are used for treating and detecting cancer in a patient, and for stimulating an immune response in patient. ABB99880-ABB99885 represent WT1 amino acid sequences of the invention.

XX ABG33402;
AC 15-JUL-2002 (first entry)
XX DE Human WT1-ubiquitin fusion construct.
XX KW Human; mouse; cytosolic; immunostimulant; WT1; cancer;
XX KW immune response.
XX OS Homo sapiens.
XX EN WO200228414-A1.
XX PD 11-APR-2002.
XX PF 03-OCT-2001; 2001WO-US311139.
XX PR 06-OCT-2000; 2000US-0684361.
XX PR 09-OCT-2000; 2000US-0685830.
XX PR 15-FEB-2001; 2001US-0785019.
XX PR 24-AUG-2001; 2001US-0938864.
XX PA (CORI-) CORIXA CORP.
XX PA (GAIG/) GAIGER A.
XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
XX PI Sleath PR, Mosman S, Evans L, Spies AG, Boydston J;
XX DR WPI: 2002-352217/38.
XX DR N-PSDB; ABK69686.
XX PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
XX PT treating and diagnosing cancer in a patient -
XX PS Claim 2; Page 257-258; 260pp; English.
XX CC The invention relates to an isolated WT1 polynucleotide (I) and
XX CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
XX CC are used for treating and detecting cancer in a patient, and for
XX CC stimulating an immune response in patient. ABG33070-ABG33405
XX CC represent WT1 amino acid sequences of the invention.
XX SQ Sequence 504 AA;
XX
XX Query Match 100.0%; Score 51; DB 23; Length 504;
XX Best Local Similarity 100.0%; Pred. No. 0.2;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PF 03-OCT-2001; 2001WO-US311139.
XX 06-OCT-2000; 2000US-0684361.
XX 09-OCT-2000; 2000US-0685830.
XX 15-FEB-2001; 2001US-0785019.
XX 24-AUG-2001; 2001US-0938864.
XX (CORI-) CORIXA CORP.
XX (GAIG/) GAIGER A.
XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
XX PI Sleath PR, Mosman S, Evans L, Spies AG, Boydston J;
XX DR WPI: 2002-352217/38.
XX DR N-PSDB; ABK69686.
XX PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
XX PT treating and diagnosing cancer in a patient -
XX PS Claim 2; Page 243-245; 260pp; English.
XX CC The invention relates to an isolated WT1 polynucleotide (I) and
XX CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
XX CC are used for treating and detecting cancer in a patient, and for
XX CC stimulating an immune response in patient. ABG33070-ABG33405
XX CC represent WT1 amino acid sequences of the invention.
XX SQ Sequence 568 AA;
XX
XX Query Match 100.0%; Score 51; DB 23; Length 568;
XX Best Local Similarity 100.0%; Pred. No. 0.23;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
Db 265 RMPFNAPYL 273

RESULT 63
AA022140
ID AA022140 standard; Protein; 577 AA.
XX AA022140;
AC
XX 03-OCT-2002 (first entry)
DT
XX Ra12-WT1 fusion protein.
DE
XX Ra12; serine protease antigen; MTRB32A; Mycobacterium tuberculosis;
XX KW vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
XX KW immunogen; cytokine.
XX OS Chimeric - Unidentified.
XX PN WO200125401-A2.
XX PD 12-APR-2001.
XX PF 06-OCT-2000; 2000WO-US227652.
XX PR 07-OCT-1999; 99US-0158585.
XX PA (CORI-) CORIXA CORP.
XX PI Skeiky Y, Guderian J;
XX DR WPI: 2001-266299/27.
XX DR N-PSDB; AALA0771.
XX PT Recombinant nucleic acid molecule for producing high yield expression
XX PT of desired fusion polypeptides, encodes fusion polypeptide comprising
XX PT Mycobacterium tuberculosis coding sequence and heterologous polypeptide

XX Disclosure: Fig 4; 39pp; English.
 CC The invention relates to a recombinant nucleic acid molecule encoding a
 CC fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14
 CC Kda C-terminal fragment of serine protease antigen M7532A of
 CC Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.
 CC The recombinant fusion nucleic acids and polypeptides are useful for
 CC providing stable and high yield expression of fusion polypeptides of both
 CC eukaryotic and prokaryotic origin and to encode a protein product for use
 CC as an antigen for detecting serum antibodies. The presence of serum
 CC antibodies to M. tuberculosis antigens in an individual indicates that
 CC the individual is infected with it. The fusion polypeptides are useful as
 CC sources of proteins for monitoring binding of serum antibodies to fusion
 CC proteins and as an immunogen to induce and/or enhance immune responses.
 CC The coding sequences can be ligated with a coding sequence of another
 CC molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and
 CC can be used in vivo as a DNA vaccine. This sequence represents the
 CC Ral2-WT1 fusion protein relating to the invention.

SO Sequence 577 AA;
 Query Match 100.0%; Score 51; DB 22; Length 577;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 275 RMPFNAPYL 283

RESULT 64
 ABG33383
 ID ABG33383 standard; Protein; 591 AA.
 AC ABG33383;
 XX 15-JUL-2002 (first entry)
 DT Human Trx.WT1.
 DE Human; mouse; cytosstatic; immunostimulant; WT1; cancer;
 KW immune response.
 XX Homo sapiens.
 OS WO200228414-A1.
 PN 11-APR-2002.
 PD 03-OCT-2001; 2001WO-US31139.
 PF 06-OCT-2000; 2000US-0684361.
 PR 09-OCT-2000; 2000US-0685830.
 PR 15-FEB-2001; 2001US-0785019.
 PR 24-AUG-2001; 2001US-0938864.
 XX (CORI-) CORIXA CORP.
 PA (GAI/) GAIGER A.
 XX Galger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
 PI Sleath PR, Mossman S, Evans L, Spies AG, Boyderson J;
 DR WPI; 2002-352217/38.
 DR N-PSDB; ABK69665.
 XX Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
 PT treating and diagnosing cancer in a patient -
 XX Claim 2; Page 22-223; 260pp; English.
 PS The invention relates to an isolated WT1 polynucleotide (I) and
 CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides

CC are used for treating and detecting cancer in a patient, and for
 CC stimulating an immune response in patient. ABG33070-ABG33405
 CC represent WT1 amino acid sequences of the invention.

SO Sequence 591 AA;
 Query Match 100.0%; Score 51; DB 23; Length 591;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 288 RMPFNAPYL 296

RESULT 65
 AAG62154
 ID AAG62154 standard; Protein; 692 AA.
 AC AAG62154;
 XX 06-JUL-2001 (first entry)
 DT Human WT1/PSA fusion protein SEQ ID NO: 357.
 DE Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;
 KW chromosome 11p13; zinc finger transcription factor.
 KM Homo sapiens.
 OS WO200125273-A2.
 PN 12-APR-2001.
 PD 04-OCT-2000; 2000WO-US27465.
 PR 04-OCT-1999; 99US-0157459.
 PR (CORI-) CORIXA CORP.
 PA (CORI-) CORIXA CORP.
 XX Skeiky YAW, Xu J, Cheever MA, Reed SG;
 DR WPI; 2001-328324/34.

PT Polypeptide comprising part of the Wilm's Tumour gene product sequence is
 PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
 PT and cancer associated with WT1 -
 XX Disclosure; Page 226-228; 228pp; English.

CC The present invention describes compositions comprising peptides derived
 CC from the Wilm's tumour protein WT1 and methods for their use in treating
 CC malignant diseases. Peptides derived from both the murine and human WT1
 CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
 CC and the protein was shown to be a zinc finger transcription factor. The
 CC immunogenic peptides of the invention are particularly useful in the
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is
 CC a polypeptide described in the exemplification of the invention.

SO Sequence 692 AA;
 Query Match 100.0%; Score 51; DB 22; Length 692;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 126 RMPFNAPYL 134

Search completed: January 21, 2004, 09:11:03
 Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 21, 2004, 09:02:27 ; Search time 33 Seconds

(Without alignments)
55,768 Million cell updates/sec

Title: US-09-625-963A-1

Perfect score: 51

Sequence: 1 RMPNAPYL 9

Scoring table: BLOSUM62

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Searched: 762491 seqs, 204481190 residues

Total number of hits satisfying chosen parameters: 179

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 500 summaries

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- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubppaa/US09C_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_NEW_PUB.pep.*
- 16: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	US-09-872-832-46	Sequence 46, App1
2	51	100.0	9	US-09-938-864-185	Sequence 185, App
3	51	100.0	9	US-09-938-864-293	Sequence 293, App
4	51	100.0	9	US-09-791-477-185	Sequence 185, App
5	51	100.0	9	US-09-791-477-293	Sequence 293, App
6	51	100.0	9	US-09-785-019-185	Sequence 185, App
7	51	100.0	9	US-09-785-019-293	Sequence 293, App
8	51	100.0	9	US-10-210-148-54	Sequence 54, App1
9	51	100.0	9	US-10-195-835-185	Sequence 185, App
10	51	100.0	9	US-10-185-835-293	Sequence 293, App
11	51	100.0	9	US-10-286-333-185	Sequence 185, App
12	51	100.0	9	US-10-286-333-293	Sequence 293, App
13	51	100.0	9	US-10-244-830-185	Sequence 185, App
14	51	100.0	9	US-10-244-830-293	Sequence 293, App
15	51	100.0	9	US-10-125-635A-185	Sequence 185, App

16	51	100.0	9	US-10-125-635A-293	Sequence 293, App
17	51	100.0	9	US-10-002-603-185	Sequence 185, App
18	51	100.0	9	US-10-002-603-293	Sequence 293, App
19	51	100.0	23	US-09-938-864-2	Sequence 2, App11
20	51	100.0	23	US-09-938-864-3	Sequence 3, App11
21	51	100.0	23	US-09-791-477-2	Sequence 2, App11
22	51	100.0	23	US-09-791-477-3	Sequence 3, App11
23	51	100.0	23	US-09-785-019-2	Sequence 2, App11
24	51	100.0	23	US-09-785-019-3	Sequence 3, App11
25	51	100.0	23	US-10-195-835-2	Sequence 2, App11
26	51	100.0	23	US-10-195-835-3	Sequence 3, App11
27	51	100.0	23	US-10-286-333-2	Sequence 2, App11
28	51	100.0	23	US-10-286-333-3	Sequence 3, App11
29	51	100.0	23	US-10-244-830-2	Sequence 2, App11
30	51	100.0	23	US-10-244-830-3	Sequence 3, App11
31	51	100.0	23	US-10-125-635A-2	Sequence 2, App11
32	51	100.0	23	US-10-125-635A-3	Sequence 3, App11
33	51	100.0	23	US-10-002-603-2	Sequence 2, App11
34	51	100.0	23	US-10-002-603-3	Sequence 3, App11
35	51	100.0	152	US-09-938-864-343	Sequence 343, App
36	51	100.0	152	US-09-785-019-343	Sequence 343, App
37	51	100.0	152	US-10-195-835-343	Sequence 343, App
38	51	100.0	152	US-10-286-333-343	Sequence 343, App
39	51	100.0	152	US-10-244-830-343	Sequence 343, App
40	51	100.0	152	US-10-125-635A-343	Sequence 343, App
41	51	100.0	152	US-10-002-603-343	Sequence 343, App
42	51	100.0	154	US-09-929-315-5	Sequence 5, App11
43	51	100.0	154	US-09-993-215-5	Sequence 5, App11
44	51	100.0	214	US-09-938-864-395	Sequence 395, App
45	51	100.0	214	US-10-195-835-395	Sequence 395, App
46	51	100.0	214	US-10-286-333-395	Sequence 395, App
47	51	100.0	214	US-10-244-830-395	Sequence 395, App
48	51	100.0	214	US-10-125-635A-395	Sequence 395, App
49	51	100.0	214	US-10-002-603-395	Sequence 395, App
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53	51	100.0	256	US-10-286-333-335	Sequence 335, App
54	51	100.0	256	US-10-244-830-335	Sequence 335, App
55	51	100.0	256	US-10-125-635A-335	Sequence 335, App
56	51	100.0	256	US-10-002-603-335	Sequence 335, App
57	51	100.0	270	US-10-286-333-478	Sequence 478, App
58	51	100.0	270	US-10-286-333-502	Sequence 502, App
59	51	100.0	274	US-10-286-333-480	Sequence 480, App
60	51	100.0	278	US-10-286-333-483	Sequence 483, App
61	51	100.0	280	US-10-195-835-461	Sequence 461, App
62	51	100.0	280	US-10-286-333-461	Sequence 461, App
63	51	100.0	280	US-10-244-830-461	Sequence 461, App
64	51	100.0	280	US-10-125-635A-461	Sequence 461, App
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66	51	100.0	281	US-10-244-830-465	Sequence 465, App
67	51	100.0	291	US-10-286-333-464	Sequence 464, App
68	51	100.0	291	US-10-244-830-464	Sequence 464, App
69	51	100.0	292	US-10-286-333-470	Sequence 470, App
70	51	100.0	292	US-10-286-333-499	Sequence 499, App
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72	51	100.0	310	US-10-286-333-481	Sequence 481, App
73	51	100.0	321	US-10-195-835-455	Sequence 455, App
74	51	100.0	321	US-10-286-333-455	Sequence 455, App
75	51	100.0	321	US-10-244-830-479	Sequence 479, App
76	51	100.0	321	US-10-125-635A-479	Sequence 479, App
77	51	100.0	321	US-10-002-603-455	Sequence 455, App
78	51	100.0	321	US-10-286-333-455	Sequence 455, App
79	51	100.0	344	US-09-938-864-391	Sequence 391, App
80	51	100.0	344	US-10-195-835-391	Sequence 391, App
81	51	100.0	344	US-10-286-333-391	Sequence 391, App
82	51	100.0	344	US-10-244-830-391	Sequence 391, App
83	51	100.0	344	US-10-125-635A-391	Sequence 391, App
84	51	100.0	345	US-10-002-603-391	Sequence 391, App
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86	51	100.0	345	US-09-993-215-2	Sequence 2, App11
87	51	100.0	352	US-09-938-864-394	Sequence 394, App
88	51	100.0	352	US-10-195-835-394	Sequence 394, App
89	51	100.0	352	US-10-286-333-394	Sequence 394, App

89 51 100.0 362 12 US-10-244-830-394 Sequence 394, App
90 51 100.0 362 15 US-10-125-635A-394 Sequence 394, App
91 51 100.0 369 11 US-10-002-603-394 Sequence 394, App
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93 51 100.0 369 12 US-09-785-019-346 Sequence 346, App
94 51 100.0 369 11 US-10-195-835-346 Sequence 346, App
95 51 100.0 369 12 US-10-286-333-346 Sequence 346, App
96 51 100.0 369 12 US-10-244-830-346 Sequence 346, App
97 51 100.0 369 15 US-10-125-635A-346 Sequence 346, App
98 51 100.0 369 15 US-10-002-603-346 Sequence 346, App
99 51 100.0 410 11 US-09-938-864-333 Sequence 333, App
100 51 100.0 410 11 US-09-785-019-333 Sequence 333, App
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103 51 100.0 410 12 US-10-244-830-333 Sequence 333, App
104 51 100.0 410 15 US-10-125-635A-333 Sequence 333, App
105 51 100.0 410 15 US-10-002-603-333 Sequence 333, App
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109 51 100.0 420 12 US-10-244-830-393 Sequence 393, App
110 51 100.0 420 15 US-10-125-635A-393 Sequence 393, App
111 51 100.0 420 15 US-10-002-603-393 Sequence 393, App
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115 51 100.0 428 12 US-10-244-830-405 Sequence 405, App
116 51 100.0 428 15 US-10-125-635A-405 Sequence 405, App
117 51 100.0 428 15 US-10-002-603-405 Sequence 405, App
118 51 100.0 429 11 US-09-938-864-408 Sequence 408, App
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120 51 100.0 429 12 US-10-286-333-408 Sequence 408, App
121 51 100.0 429 12 US-10-244-830-408 Sequence 408, App
122 51 100.0 429 15 US-10-125-635A-408 Sequence 408, App
123 51 100.0 429 15 US-10-002-603-408 Sequence 408, App
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125 51 100.0 449 10 US-09-993-215-4 Sequence 4, Appli
126 51 100.0 449 10 US-09-993-215-6 Sequence 6, Appli
127 51 100.0 449 11 US-09-938-864-319 Sequence 319, App
128 51 100.0 449 11 US-09-938-864-320 Sequence 320, App
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130 51 100.0 449 11 US-09-938-864-404 Sequence 319, App
131 51 100.0 449 11 US-09-791-477-319 Sequence 320, App
132 51 100.0 449 11 US-09-791-477-320 Sequence 319, App
133 51 100.0 449 11 US-09-785-019-319 Sequence 319, App
134 51 100.0 449 11 US-09-785-019-320 Sequence 320, App
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136 51 100.0 449 12 US-10-195-835-319 Sequence 319, App
137 51 100.0 449 12 US-10-195-835-320 Sequence 320, App
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143 51 100.0 449 12 US-10-244-830-320 Sequence 320, App
144 51 100.0 449 12 US-10-244-830-404 Sequence 404, App
145 51 100.0 449 15 US-10-125-635A-319 Sequence 319, App
146 51 100.0 449 15 US-10-125-635A-320 Sequence 320, App
147 51 100.0 449 15 US-10-125-635A-404 Sequence 404, App
148 51 100.0 449 15 US-10-002-603-319 Sequence 319, App
149 51 100.0 449 15 US-10-002-603-320 Sequence 320, App
150 51 100.0 449 15 US-10-002-603-404 Sequence 404, App
151 51 100.0 469 12 US-10-195-835-454 Sequence 454, App
152 51 100.0 469 12 US-10-286-333-454 Sequence 454, App
153 51 100.0 469 12 US-10-244-830-454 Sequence 454, App
154 51 100.0 469 15 US-10-125-635A-454 Sequence 454, App
155 51 100.0 495 11 US-09-938-864-409 Sequence 409, App
156 51 100.0 495 12 US-10-195-835-409 Sequence 409, App
157 51 100.0 495 12 US-10-286-333-409 Sequence 409, App
158 51 100.0 495 12 US-10-244-830-409 Sequence 409, App
159 51 100.0 495 15 US-10-125-635A-409 Sequence 409, App
160 51 100.0 495 15 US-10-002-603-409 Sequence 409, App
161 51 100.0 504 11 US-09-938-864-410 Sequence 410, App

162 51 100.0 504 12 US-10-195-835-410 Sequence 410, App
163 51 100.0 504 12 US-10-286-333-410 Sequence 410, App
164 51 100.0 504 12 US-10-244-830-410 Sequence 410, App
165 51 100.0 504 15 US-10-125-635A-410 Sequence 410, App
166 51 100.0 504 15 US-10-002-603-410 Sequence 410, App
167 51 100.0 568 11 US-09-938-864-392 Sequence 392, App
168 51 100.0 568 12 US-10-195-835-392 Sequence 392, App
169 51 100.0 568 12 US-10-286-333-392 Sequence 392, App
170 51 100.0 568 12 US-10-244-830-392 Sequence 392, App
171 51 100.0 568 15 US-10-125-635A-392 Sequence 392, App
172 51 100.0 591 11 US-09-938-864-334 Sequence 334, App
173 51 100.0 591 11 US-09-785-019-334 Sequence 334, App
174 51 100.0 591 12 US-10-195-835-334 Sequence 334, App
175 51 100.0 591 12 US-10-286-333-334 Sequence 334, App
176 51 100.0 591 12 US-10-244-830-334 Sequence 334, App
177 51 100.0 591 12 US-10-125-635A-334 Sequence 334, App
178 51 100.0 591 15 US-10-002-603-334 Sequence 334, App
179 51 100.0 591 15 US-10-002-603-334 Sequence 334, App

ALIGNMENTS

RESULT 1
US-09-872-832-46
; Sequence 46, Application US/09872832
; Patent No. US20020131960A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Cancer Center
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 830002-2003.1
; CURRENT APPLICATION NUMBER: US/09/872,832
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/209,157
; PRIOR FILING DATE: 2000-02-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-832-46

Query Match 100.0%; DB 10: Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMPFNAPYL 9
|||
Db 1 RMPFNAPYL 9

RESULT 2
US-09-938-864-185
; Sequence 185, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smitthall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spiles, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTL
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465CS
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413

Db 1 RMPFNAPYL 9

RESULT 7

US-09-785-019-293
 ; Sequence 293, Application US/09785019
 ; Publication No. US20030082196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smithgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Sleach, Paul
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C4
 ; CURRENT FILING DATE: 2001-02-15
 ; NUMBER OF SEQ ID NOS: 376
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 293
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-785-019-293

Query Match 100.0%; Score 51; DB 11; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9

RESULT 8

US-10-210-148-54
 ; Sequence 54, Application US/10210148
 ; Publication No. US20030171280A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Soderstrom, Karl Petter
 ; TITLE OF INVENTION: Compositions And Methods For Modulation Of Immune Response
 ; FILE REFERENCE: TROM0002
 ; CURRENT APPLICATION NUMBER: US/10/210.148
 ; CURRENT FILING DATE: 2002-07-31
 ; PRIOR APPLICATION NUMBER: PCT/US02/24311
 ; PRIOR FILING DATE: 2002-07-31
 ; NUMBER OF SEQ ID NOS: 117
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 54
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-210-148-54

Query Match 100.0%; Score 51; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9

RESULT 9

US-10-195-835-185
 ; Sequence 185, Application US/10195835
 ; Publication No. US20030198622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Smithgall, Molly D.

Db 1 RMPFNAPYL 9

APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; APPLICANT: Mossman, Sally P.
 ; APPLICANT: Evans, Lawrence S.
 ; APPLICANT: Swanson, Ryan M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C8
 ; CURRENT APPLICATION NUMBER: US/10/195.835
 ; CURRENT FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 185
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-195-835-185

Query Match 100.0%; Score 51; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9

RESULT 10

US-10-195-835-293
 ; Sequence 293, Application US/10195835
 ; Publication No. US20030198622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; APPLICANT: Mossman, Sally P.
 ; APPLICANT: Evans, Lawrence S.
 ; APPLICANT: Swanson, Ryan M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C8
 ; CURRENT APPLICATION NUMBER: US/10/195.835
 ; CURRENT FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 293
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-195-835-293

Query Match 100.0%; Score 51; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9

RESULT 11

US-10-286-333-185
 ; Sequence 185, Application US/10286333
 ; Publication No. US20030215458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Jaya, No. US20030215458A1a11e

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286.333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-286-333-185

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Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

```

```

RESULT 12
US-10-286-333-293
; Sequence 293, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286.333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-286-333-293

```

```

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

```

```

RESULT 13
US-10-244-830-185
; Sequence 185, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244.830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-244-830-185

```

```

Query Match      100.0%; Score 51; DB 12; Length 9;

```

```

Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

```

```

RESULT 14
US-10-244-830-293
; Sequence 293, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244.830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-244-830-293

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```

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

```

```

RESULT 15
US-10-125-635A-185
; Sequence 185, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Derrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125.635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-125-635A-185

```

```

Query Match      100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

```

```

RESULT 16
US-10-125-635A-293
; Sequence 293, Application US/10125635A

```

```

; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125.635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-125-635A-293

```

```

Query Match          100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

```

```

RESULT 17
US-10-002-603-185
; Sequence 185, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002.603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-002-603-185

```

```

Query Match          100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

```

```

RESULT 18
US-10-002-603-293
; Sequence 293, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander

```

```

; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002.603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-002-603-293

```

```

Query Match          100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

```

```

RESULT 19
US-09-938-864-2
; Sequence 2, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938.864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-2

```

```

Query Match          100.0%; Score 51; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
Db 10 RMPFNAPYL 18

```

```

RESULT 20
US-09-938-864-3
; Sequence 3, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-938-864-3

```

```

Query Match          100.0%; Score 51; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
Db 10 RMPFNAPYL 18

```

```

RESULT 21
US-09-791-477-2
; Sequence 2, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-2

```

```

Query Match          100.0%; Score 51; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
Db 10 RMPFNAPYL 18

```

```

RESULT 22
US-09-791-477-3
; Sequence 3, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200

```

```

; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-477-3

```

```

Query Match          100.0%; Score 51; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
Db 10 RMPFNAPYL 18

```

```

RESULT 23
US-09-785-019-2
; Sequence 2, Application US/09785019
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-2

```

```

Query Match          100.0%; Score 51; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RMPFNAPYL 9
Db 10 RMPFNAPYL 18

```

```

RESULT 24
US-09-785-019-3
; Sequence 3, Application US/09785019
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376

```

```

SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-785-019-3

```

```

Query Match          100.0%; Score 51; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMFPNAPYL 9
   |||||
Db 10 RMFPNAPYL 18

```

```

RESULT 25
US-10-195-835-2
; Sequence 2, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smilthgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Moseman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C8
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-195-835-2

```

```

Query Match          100.0%; Score 51; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMFPNAPYL 9
   |||||
Db 10 RMFPNAPYL 18

```

```

RESULT 26
US-10-195-835-3
; Sequence 3, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smilthgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Moseman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C8
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0

```

```

; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-195-835-3

```

```

Query Match          100.0%; Score 51; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMFPNAPYL 9
   |||||
Db 10 RMFPNAPYL 18

```

```

RESULT 27
US-10-286-333-2
; Sequence 2, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20030215458A1a11e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-286-333-2

```

```

Query Match          100.0%; Score 51; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMFPNAPYL 9
   |||||
Db 10 RMFPNAPYL 18

```

```

RESULT 28
US-10-286-333-3
; Sequence 3, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20030215458A1a11e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-286-333-3

```

```

Query Match          100.0%; Score 51; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMFPNAPYL 9
   |||||
Db 10 RMFPNAPYL 18

```

RESULT 29
 US-10-244-830-2
 ; Sequence 2, Application US/10244830
 ; Publication No. US20030235557A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Cheever, Martin A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C9
 ; CURRENT APPLICATION NUMBER: US/10/244.830
 ; CURRENT FILING DATE: 2002-09-16
 ; NUMBER OF SEQ ID NOS: 468
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 23
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-244-830-2

Query Match 100.0%; Score 51; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 10 RMPFNAPYL 18

RESULT 30
 US-10-244-830-3
 ; Sequence 3, Application US/10244830
 ; Publication No. US20030235557A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Cheever, Martin A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C9
 ; CURRENT APPLICATION NUMBER: US/10/244.830
 ; CURRENT FILING DATE: 2002-09-16
 ; NUMBER OF SEQ ID NOS: 468
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 23
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-244-830-3

Query Match 100.0%; Score 51; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 10 RMPFNAPYL 18

RESULT 31
 US-10-125-635A-2
 ; Sequence 2, Application US/10125635A
 ; Publication No. US20030039635A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; CURRENT FILING DATE: 2001-10-30

FILE REFERENCE: 210121.465C7
 ; CURRENT APPLICATION NUMBER: US/10/125.635A
 ; CURRENT FILING DATE: 2002-07-19
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 23
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-125-635A-2

Query Match 100.0%; Score 51; DB 15; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 10 RMPFNAPYL 18

RESULT 32
 US-10-125-635A-3
 ; Sequence 3, Application US/10125635A
 ; Publication No. US20030039635A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C7
 ; CURRENT APPLICATION NUMBER: US/10/125.635A
 ; CURRENT FILING DATE: 2002-07-19
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 23
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-125-635A-3

Query Match 100.0%; Score 51; DB 15; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 10 RMPFNAPYL 18

RESULT 33
 US-10-002-603-2
 ; Sequence 2, Application US/10002603
 ; Publication No. US20030095971A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smithgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedavick, Thomas S.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Mosman, Sally
 ; APPLICANT: Evans, Lawrence
 ; APPLICANT: Spies, A. Gregory
 ; APPLICANT: Boydston, Jeremy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C6
 ; CURRENT APPLICATION NUMBER: US/10/002.603
 ; CURRENT FILING DATE: 2001-10-30

```

; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-002-603-2

```

```

Query Match          100.0%; Score 51; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RMPFNAPYL 9
Db 10 RMPFNAPYL 18

```

```

RESULT 34
US-10-002-603-3
; Sequence 3, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-002-603-3

```

```

Query Match          100.0%; Score 51; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RMPFNAPYL 9
Db 10 RMPFNAPYL 18

```

```

RESULT 35
US-09-938-864-343
; Sequence 343, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864

```

```

; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-864-343

```

```

Query Match          100.0%; Score 51; DB 11; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RMPFNAPYL 9
Db 51 RMPFNAPYL 59

```

```

RESULT 36
US-09-785-019-343
; Sequence 343, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-019-343

```

```

Query Match          100.0%; Score 51; DB 11; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RMPFNAPYL 9
Db 51 RMPFNAPYL 59

```

```

RESULT 37
US-10-195-835-343
; Sequence 343, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Mossman, Sally P.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/195,835
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0

```

```

; SEQ ID NO 343
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-835-343

```

```

Query Match      100.0%; Score 51; DB 12; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
      |||
      51 RMPFNAPYL 59

```

```

RESULT 38
US-10-286-333-343
; Sequence 343, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-343

```

```

Query Match      100.0%; Score 51; DB 12; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
      |||
      51 RMPFNAPYL 59

```

```

RESULT 39
US-10-244-830-343
; Sequence 343, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244,830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-244-830-343

```

```

Query Match      100.0%; Score 51; DB 12; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
      |||
      51 RMPFNAPYL 59

```

```

RESULT 40
US-10-125-635A-343
; Sequence 343, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Gaiger, Alexander
; APPLICANT: Sattgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-343

```

```

Query Match      100.0%; Score 51; DB 15; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
      |||
      51 RMPFNAPYL 59

```

```

RESULT 41
US-10-002-603-343
; Sequence 343, Application US/10002603
; Publication No. US930030095971A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smtgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Steath, Paul R.
; APPLICANT: Kossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-603-343

```

```

Query Match      100.0%; Score 51; DB 15; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
      |||
      51 RMPFNAPYL 59

```

```

RESULT 42
US-09-929-315-5

```

```

Sequence 5, Application US/09929315
Patent No. US20020082394A1
GENERAL INFORMATION:
APPLICANT: Call, Katherine M.
APPLICANT: Glaser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Houseman, David E.
APPLICANT: Bruening, Wendy
APPLICANT: Darveau, Andre
TITLE OF INVENTION: Localization and Characterization of the
FILE REFERENCE: 0050.1312-013
CURRENT APPLICATION NUMBER: US/09/929,315
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 09/037,179
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 08/102,942
PRIOR FILING DATE: 1993-08-02
PRIOR APPLICATION NUMBER: US 07/614,161
PRIOR FILING DATE: 1990-11-13
PRIOR APPLICATION NUMBER: US 07/435,780
PRIOR FILING DATE: 1989-11-13
PRIOR APPLICATION NUMBER: US 07/795,323
PRIOR FILING DATE: 1991-11-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 154
TYPE: PRT
ORGANISM: Homo sapien
US-09-929-315-5

```

```

Query Match 100.0%; Score 51; DB 9; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
Db 40 RMPFNAPYL 48

RESULT 43
US-09-993-215-5
Sequence 5, Application US/09993215
Patent No. US20020128196A1
GENERAL INFORMATION:
APPLICANT: Call, Katherine M.
APPLICANT: Glaser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Houseman, David E.
APPLICANT: Bruening, Wendy
APPLICANT: Darveau, Andre
TITLE OF INVENTION: Localization and Characterization of the
FILE REFERENCE: 0050.1312-014
CURRENT APPLICATION NUMBER: US/09/993,215
CURRENT FILING DATE: 2001-11-12
PRIOR APPLICATION NUMBER: US 09/037,179
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 08/102,942
PRIOR FILING DATE: 1993-08-02
PRIOR APPLICATION NUMBER: US 07/614,161
PRIOR FILING DATE: 1990-11-13
PRIOR APPLICATION NUMBER: US 07/435,780
PRIOR FILING DATE: 1989-11-13

```

```

PRIOR APPLICATION NUMBER: US 07/795,323
PRIOR FILING DATE: 1991-11-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 154
TYPE: PRT
ORGANISM: Homo sapien
US-09-993-215-5

```

```

Query Match 100.0%; Score 51; DB 10; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
Db 40 RMPFNAPYL 48

```

```

RESULT 44
US-09-938-864-395
Sequence 395, Application US/09938864
Publication No. US20030072767A1
GENERAL INFORMATION:
APPLICANT: Galdier, Alexander
APPLICANT: McNeill, Patricia D.
APPLICANT: Smitngall, Molly
APPLICANT: Moulton, Gus
APPLICANT: Vedvick, Thomas S.
APPLICANT: Sleath, Paul R.
APPLICANT: Mossman, Sally
APPLICANT: Evans, Lawrence
APPLICANT: Spies, A. Gregory
APPLICANT: Boydston, Jeremy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTL
FILE REFERENCE: 210121.465C5
CURRENT APPLICATION NUMBER: US/09/938,864
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 413
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 395
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapiens
US-09-938-864-395

```

```

Query Match 100.0%; Score 51; DB 11; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
Db 59 RMPFNAPYL 67

```

```

RESULT 45
US-10-195-835-395
Sequence 395, Application US/10195835
Publication No. US20030198622A1
GENERAL INFORMATION:
APPLICANT: Galdier, Alexander
APPLICANT: Smitngall, Molly D.
APPLICANT: Carter, Darrick
APPLICANT: Cheever, Martin A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Sutherland, R. Alec
APPLICANT: Mossman, Sally P.
APPLICANT: Evans, Lawrence S.
APPLICANT: Swanson, Ryan M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTL
FILE REFERENCE: 210121.465C8

```

```

; CURRENT APPLICATION NUMBER: US/10/195,835
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 395
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-835-395

```

```

Query Match          100.0%; Score 51; DB 12; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RMPFNAPYL 9
Db 59 RMPFNAPYL 67

```

```

RESULT 46
US-10-286-333-395
; Sequence 395, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 395
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-395

```

```

Query Match          100.0%; Score 51; DB 12; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RMPFNAPYL 9
Db 59 RMPFNAPYL 67

```

```

RESULT 47
US-10-244-830-395
; Sequence 395, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244,830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 395
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-244-830-395

```

```

Query Match          100.0%; Score 51; DB 12; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RMPFNAPYL 9
Db 59 RMPFNAPYL 67

```

```

RESULT 48
US-10-125-635A-395
; Sequence 395, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 395
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-395

```

```

Query Match          100.0%; Score 51; DB 15; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RMPFNAPYL 9
Db 59 RMPFNAPYL 67

```

```

RESULT 49
US-10-002-603-395
; Sequence 395, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 395
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-603-395

```

```

Query Match          100.0%; Score 51; DB 15; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RMPFNAPYL 9
Db 59 RMPFNAPYL 67

```

RESULT 50
 US-09-938-864-335
 ; Sequence 335, Application US/09938864
 ; Publication No. US20030072767N1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smithgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Mossman, Sally
 ; APPLICANT: Evans, Lawrence
 ; APPLICANT: Spies, A. Gregory
 ; APPLICANT: Boydston, Jeremy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 ; FILE REFERENCE: 210121.465C5
 ; CURRENT APPLICATION NUMBER: US/09/938, 864
 ; CURRENT FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 335
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-938-864-335

Query Match 100.0%; Score 51; DB 11; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.22; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

OY 1 RMPFNAPYL 9
 |||||
 Db 133 RMPFNAPYL 141

RESULT 51
 US-09-785-019-335
 ; Sequence 335, Application US/09785019
 ; Publication No. US20030082196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smithgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Sleath, Paul
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 ; FILE REFERENCE: 210121.465C4
 ; CURRENT APPLICATION NUMBER: US/09/785, 019
 ; CURRENT FILING DATE: 2001-02-15
 ; NUMBER OF SEQ ID NOS: 376
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 335
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-785-019-335

Query Match 100.0%; Score 51; DB 11; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.22; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

OY 1 RMPFNAPYL 9
 |||||
 Db 133 RMPFNAPYL 141

RESULT 52
 US-10-195-835-335
 ; Sequence 335, Application US/10195835
 ; Publication No. US20030198622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; APPLICANT: Mossman, Sally P.
 ; APPLICANT: Evans, Lawrence S.
 ; APPLICANT: Swanson, Ryan M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 ; FILE REFERENCE: 210121.465C8
 ; CURRENT APPLICATION NUMBER: US/10/195, 835
 ; CURRENT FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 335
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-195-835-335

Query Match 100.0%; Score 51; DB 12; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.22; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

OY 1 RMPFNAPYL 9
 |||||
 Db 133 RMPFNAPYL 141

RESULT 53
 US-10-286-333-335
 ; Sequence 335, Application US/10286333
 ; Publication No. US20030215458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Jeva, No. US20030215458A1a1e
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 ; FILE REFERENCE: 210121.465C10
 ; CURRENT APPLICATION NUMBER: US/10/286, 333
 ; CURRENT FILING DATE: 2002-10-30
 ; NUMBER OF SEQ ID NOS: 506
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 335
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-286-333-335

Query Match 100.0%; Score 51; DB 12; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.22; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

OY 1 RMPFNAPYL 9
 |||||
 Db 133 RMPFNAPYL 141

RESULT 54
 US-10-244-830-335
 ; Sequence 335, Application US/10244830
 ; Publication No. US20030235557A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Cheever, Martin A.

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244,830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-244-830-335

```

```

Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 256;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RMPFNAPYL 9
Db 133 RMPFNAPYL 141

```

```

RESULT 55
US-10-125-635A-335
; Sequence 335, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-335

```

```

Query Match
Best Local Similarity 100.0%; Score 51; DB 15; Length 256;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RMPFNAPYL 9
Db 133 RMPFNAPYL 141

```

```

RESULT 56
US-10-002-603-335
; Sequence 335, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spires, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6

```

```

; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-603-335

```

```

Query Match
Best Local Similarity 100.0%; Score 51; DB 15; Length 256;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RMPFNAPYL 9
Db 133 RMPFNAPYL 141

```

```

RESULT 57
US-10-286-333-478
; Sequence 478, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Taya, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 478
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-478

```

```

Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 267;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RMPFNAPYL 9
Db 112 RMPFNAPYL 120

```

```

RESULT 58
US-10-286-333-502
; Sequence 502, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Taya, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 502
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-502

```

```

Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 270;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 1 RMPFNAPYL 9
 Db 115 RMPFNAPYL 123

RESULT 59
 US-10-286-333-480
 ; Sequence 480, Application US/10286333
 ; Publication No. US20030215458A1
 ; GENERAL INFORMATION:

APPLICANT: Galger, Alexander
 APPLICANT: McNeill, Patricia D
 APPLICANT: Jaya, No. US20030215458A1a1e
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 FILE REFERENCE: 210121.465C10
 CURRENT APPLICATION NUMBER: US/10/286,333
 CURRENT FILING DATE: 2002-10-30
 NUMBER OF SEQ ID NOS: 506
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 480
 LENGTH: 274
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-286-333-480

Query Match 100.0%; Score 51; DB 12; Length 274;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 Db 119 RMPFNAPYL 127

RESULT 60
 US-10-286-333-483
 ; Sequence 483, Application US/10286333
 ; Publication No. US20030215458A1
 ; GENERAL INFORMATION:

APPLICANT: Galger, Alexander
 APPLICANT: McNeill, Patricia D
 APPLICANT: Jaya, No. US20030215458A1a1e
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 FILE REFERENCE: 210121.465C10
 CURRENT APPLICATION NUMBER: US/10/286,333
 CURRENT FILING DATE: 2002-10-30
 NUMBER OF SEQ ID NOS: 506
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 483
 LENGTH: 278
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-286-333-483

Query Match 100.0%; Score 51; DB 12; Length 278;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 Db 123 RMPFNAPYL 131

RESULT 61
 US-10-195-835-461
 ; Sequence 461, Application US/10195835
 ; Publication No. US20030198622A1
 ; GENERAL INFORMATION:

APPLICANT: Galger, Alexander
 APPLICANT: Smithgall, Molly D.

APPLICANT: Carter, Darrick
 APPLICANT: Cheever, Martin A.
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Sutherland, R. Alec
 APPLICANT: Mossman, Sally P.
 APPLICANT: Evans, Lawrence S.
 APPLICANT: Swanson, Ryan M.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 FILE REFERENCE: 210121.465C8
 CURRENT APPLICATION NUMBER: US/10/195,835
 CURRENT FILING DATE: 2002-07-12
 NUMBER OF SEQ ID NOS: 461
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 461
 LENGTH: 280
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-195-835-461

Query Match 100.0%; Score 51; DB 12; Length 280;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 Db 125 RMPFNAPYL 133

RESULT 62
 US-10-286-333-461
 ; Sequence 461, Application US/10286333
 ; Publication No. US20030215458A1
 ; GENERAL INFORMATION:

APPLICANT: Galger, Alexander
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Jaya, No. US20030215458A1a1e
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 FILE REFERENCE: 210121.465C10
 CURRENT APPLICATION NUMBER: US/10/286,333
 CURRENT FILING DATE: 2002-10-30
 NUMBER OF SEQ ID NOS: 506
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 461
 LENGTH: 280
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-286-333-461

Query Match 100.0%; Score 51; DB 12; Length 280;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 Db 125 RMPFNAPYL 133

RESULT 63
 US-10-244-830-461
 ; Sequence 461, Application US/10244830
 ; Publication No. US20030235557A1
 ; GENERAL INFORMATION:

APPLICANT: Galger, Alexander
 APPLICANT: Cheever, Martin A.
 APPLICANT: Jaya, No. US20030235557A1a1e
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 FILE REFERENCE: 210121.465C9
 CURRENT APPLICATION NUMBER: US/10/244,830
 CURRENT FILING DATE: 2002-09-16
 NUMBER OF SEQ ID NOS: 468
 SOFTWARE: FastSeq for Windows Version 3.0

```

; SEQ ID NO 461
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-244-830-461

```

```

Query Match          100.0%; Score 51; DB 12; Length 280;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
      |||||
Db      125 RMPFNAPYL 133

```

```

RESULT 64
US-10-125-635A-461
; Sequence 461, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125.635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 461
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-461

```

```

Query Match          100.0%; Score 51; DB 15; Length 280;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
      |||||
Db      125 RMPFNAPYL 133

```

```

RESULT 65
US-10-286-333-465
; Sequence 465, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286.333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 465
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-465

```

```

Query Match          100.0%; Score 51; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
      |||||
Db      126 RMPFNAPYL 134

```

```

RESULT 66
US-10-244-830-465
; Sequence 465, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244.830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 465
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-244-830-465

```

```

Query Match          100.0%; Score 51; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
      |||||
Db      126 RMPFNAPYL 134

```

```

RESULT 67
US-10-286-333-464
; Sequence 464, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286.333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 464
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-464

```

```

Query Match          100.0%; Score 51; DB 12; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
      |||||
Db      126 RMPFNAPYL 134

```

```

RESULT 68
US-10-244-830-464
; Sequence 464, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY

```

```

FILE REFERENCE: 210121.465C9
CURRENT APPLICATION NUMBER: US/10/244.830
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 468
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 464
LENGTH: 291
TYPE: PRT
ORGANISM: Homo sapiens
US-10-244-830-464

```

```

Query Match          100.0%; Score 51; DB 12; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
Db      126 RMPFNAPYL 134

```

```

RESULT 69
US-10-286-333-470
Sequence 470, Application US/10286333
Publication No. US20030215458A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
FILE REFERENCE: 210121.465C10
CURRENT APPLICATION NUMBER: US/10/286.333
CURRENT FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 470
LENGTH: 292
TYPE: PRT
ORGANISM: Homo sapiens
US-10-286-333-470

```

```

Query Match          100.0%; Score 51; DB 12; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
Db      137 RMPFNAPYL 145

```

```

RESULT 70
US-10-286-333-499
Sequence 499, Application US/10286333
Publication No. US20030215458A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
FILE REFERENCE: 210121.465C10
CURRENT APPLICATION NUMBER: US/10/286.333
CURRENT FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 499
LENGTH: 292
TYPE: PRT
ORGANISM: Homo sapiens
US-10-286-333-499

```

```

Query Match          100.0%; Score 51; DB 12; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.25;

```

```

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 RMPFNAPYL 9
Db      137 RMPFNAPYL 145

```

```

RESULT 71
US-10-286-333-482
Sequence 482, Application US/10286333
Publication No. US20030215458A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
FILE REFERENCE: 210121.465C10
CURRENT APPLICATION NUMBER: US/10/286.333
CURRENT FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 482
LENGTH: 307
TYPE: PRT
ORGANISM: Homo sapiens
US-10-286-333-482

```

```

Query Match          100.0%; Score 51; DB 12; Length 307;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
Db      152 RMPFNAPYL 160

```

```

RESULT 72
US-10-286-333-481
Sequence 481, Application US/10286333
Publication No. US20030215458A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
FILE REFERENCE: 210121.465C10
CURRENT APPLICATION NUMBER: US/10/286.333
CURRENT FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 481
LENGTH: 310
TYPE: PRT
ORGANISM: Homo sapiens
US-10-286-333-481

```

```

Query Match          100.0%; Score 51; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
Db      155 RMPFNAPYL 163

```

```

RESULT 73
US-10-195-835-455
Sequence 455, Application US/10195835
Publication No. US20030198622A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander

```

```

; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick A.
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Mossman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/195,835
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 455
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-835-455

```

```

Query Match          100.0%; Score 51; DB 12; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
Db 166 RMPFNAPYL 174

RESULT 74
US-10-286-333-455
; Sequence 455, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 455
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-455

```

```

Query Match          100.0%; Score 51; DB 12; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 479
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-479

```

```

Query Match          100.0%; Score 51; DB 12; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
Db 166 RMPFNAPYL 174

RESULT 76
US-10-244-830-455
; Sequence 455, Application US/10244830
; Publication No. US2003023557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244,830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 455
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-244-830-455

```

```

Query Match          100.0%; Score 51; DB 12; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
Db 166 RMPFNAPYL 174

RESULT 77
US-10-125-635A-455
; Sequence 455, Application US/10125635A
; Publication No. US2003039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick A.
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 455
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-455

```

```

Query Match          100.0%; Score 51; DB 15; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 1 RMPFNAPYL 9
 |||||
 Db 166 RMPFNAPYL 174

RESULT 78

US-09-938-864-391
 ; Sequence 391, Application US/09938864
 ; Publication No. US2003007267A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smithgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Mosman, Sally
 ; APPLICANT: Evans, Lawrence
 ; APPLICANT: Spies, A. Gregory
 ; APPLICANT: Boydston, Jeremy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
 ; FILE REFERENCE: 210121.465C5
 ; CURRENT APPLICATION NUMBER: US/09/938,864
 ; CURRENT FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 391
 ; LENGTH: 344
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-938-864-391

Query Match 100.0%; Score 51; DB 11; Length 344;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 189 RMPFNAPYL 197

RESULT 79

US-10-195-835-391
 ; Sequence 391, Application US/10195835
 ; Publication No. US20030198622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick A.
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; APPLICANT: Mosman, Sally P.
 ; APPLICANT: Evans, Lawrence S.
 ; APPLICANT: Swanson, Ryan W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
 ; FILE REFERENCE: 210121.465C8
 ; CURRENT APPLICATION NUMBER: US/10/195,835
 ; CURRENT FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 391
 ; LENGTH: 344
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-195-835-391

Query Match 100.0%; Score 51; DB 12; Length 344;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 189 RMPFNAPYL 197

RESULT 80

US-10-286-333-391
 ; Sequence 391, Application US/10286333
 ; Publication No. US20030215458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Java, No. US20030215458A1a1e
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
 ; FILE REFERENCE: 210121.465C10
 ; CURRENT APPLICATION NUMBER: US/10/286,333
 ; CURRENT FILING DATE: 2002-10-30
 ; NUMBER OF SEQ ID NOS: 506
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 391
 ; LENGTH: 344
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-286-333-391

Query Match 100.0%; Score 51; DB 12; Length 344;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 189 RMPFNAPYL 197

RESULT 81

US-10-244-830-391
 ; Sequence 391, Application US/10244830
 ; Publication No. US20030235557A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Cheever, Martin A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
 ; FILE REFERENCE: 210121.465C9
 ; CURRENT APPLICATION NUMBER: US/10/244,830
 ; CURRENT FILING DATE: 2002-09-16
 ; NUMBER OF SEQ ID NOS: 468
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 391
 ; LENGTH: 344
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-244-830-391

Query Match 100.0%; Score 51; DB 12; Length 344;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 189 RMPFNAPYL 197

RESULT 82

US-10-125-635A-391
 ; Sequence 391, Application US/10125635A
 ; Publication No. US2003039635A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick

Query Match 100.0%; Score 51; DB 12; Length 344;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 51; DB 10; Length 345;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
 |||||
 Db 42 RMPFNAPYL 50

RESULT 86
 US-09-938-864-394
 ; Sequence 394, Application US/09938864
 ; Publication No. US2003007267A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smithgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Moegman, Sally
 ; APPLICANT: Evans, Lawrence
 ; APPLICANT: Spies, A. Gregory
 ; APPLICANT: Boydston, Jeremy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
 ; FILE REFERENCE: 210121.465C5
 ; CURRENT APPLICATION NUMBER: US/09/938,864
 ; CURRENT FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 394
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-938-864-394

Query Match 100.0%; Score 51; DB 11; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
 |||||
 Db 59 RMPFNAPYL 67

RESULT 87
 US-10-195-835-394
 ; Sequence 394, Application US/10195835
 ; Publication No. US20030198622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Derrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; APPLICANT: Moegman, Sally P.
 ; APPLICANT: Evans, Lawrence S.
 ; APPLICANT: Swanson, Ryan M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
 ; FILE REFERENCE: 210121.465C8
 ; CURRENT APPLICATION NUMBER: US/10/195,835
 ; CURRENT FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 394
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-195-835-394

Query Match 100.0%; Score 51; DB 12; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
 |||||
 Db 59 RMPFNAPYL 67

RESULT 88
 US-10-286-333-394
 ; Sequence 394, Application US/10286333
 ; Publication No. US20030215458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Jaya, No. US20030215458A1a1e
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
 ; FILE REFERENCE: 210121.465C10
 ; CURRENT APPLICATION NUMBER: US/10/286,333
 ; CURRENT FILING DATE: 2002-10-30
 ; NUMBER OF SEQ ID NOS: 506
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 394
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-286-333-394

Query Match 100.0%; Score 51; DB 12; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
 |||||
 Db 59 RMPFNAPYL 67

RESULT 89
 US-10-244-830-394
 ; Sequence 394, Application US/10244830
 ; Publication No. US20030235557A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Cheever, Martin A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
 ; FILE REFERENCE: 210121.465C9
 ; CURRENT APPLICATION NUMBER: US/10/244,830
 ; CURRENT FILING DATE: 2002-09-16
 ; NUMBER OF SEQ ID NOS: 468
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 394
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-244-830-394

Query Match 100.0%; Score 51; DB 12; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
 |||||
 Db 59 RMPFNAPYL 67

RESULT 90
 US-10-125-635A-394
 ; Sequence 394, Application US/10125635A
 ; Publication No. US20030039635A1

```

; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125.635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 394
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-394

```

```

Query Match      100.0%; Score 51; DB 15; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
        |||||||
Db      59 RMPFNAPYL 67

```

```

RESULT 91
US-10-002-603-394
; Sequence 394, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002.603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 394
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-603-394

```

```

Query Match      100.0%; Score 51; DB 15; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
        |||||||
Db      59 RMPFNAPYL 67

```

```

RESULT 92
US-09-938-864-346
; Sequence 346, Application US/09938864
; Publication No. US2003007267A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.

```

```

; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938.864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 346
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-864-346

```

```

Query Match      100.0%; Score 51; DB 11; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
        |||||||
Db      66 RMPFNAPYL 74

```

```

RESULT 93
US-09-785-019-346
; Sequence 346, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785.019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 346
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-019-346

```

```

Query Match      100.0%; Score 51; DB 11; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RMPFNAPYL 9
        |||||||
Db      66 RMPFNAPYL 74

```

```

RESULT 94
US-10-195-835-346
; Sequence 346, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.

```

```

; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Moseman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/195.835
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 346
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-835-346

```

```

Query Match      100.0%; Score 51; DB 12; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
    |||||
Db 66 RMPFNAPYL 74

RESULT 95
US-10-286-333-346
; Sequence 346, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286.333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 346
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-346

```

```

Query Match      100.0%; Score 51; DB 12; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
    |||||
Db 66 RMPFNAPYL 74

```

```

RESULT 96
US-10-244-830-346
; Sequence 346, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244.830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 346
; LENGTH: 369

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-244-830-346

```

```

Query Match      100.0%; Score 51; DB 12; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
    |||||
Db 66 RMPFNAPYL 74

```

```

RESULT 97
US-10-125-635A-346
; Sequence 346, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125.635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 346
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-346

```

```

Query Match      100.0%; Score 51; DB 15; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
    |||||
Db 66 RMPFNAPYL 74

```

```

RESULT 98
US-10-002-603-346
; Sequence 346, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Moseman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Splies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002.603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 346
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-603-346

```

Query Match 100.0%; Score 51; DB 15; Length 369;
 Best Local Similarity 100.0%; Pred. No. 0.32; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 99
 US-09-938-864-333
 ; Sequence 333, Application US/09938864
 ; Publication No. US20030072767A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smilthgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Mossman, Sally
 ; APPLICANT: Evans, Lawrence
 ; APPLICANT: Spies, A. Gregory
 ; APPLICANT: Boydston, Jeremy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C5
 ; CURRENT FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 333
 ; LENGTH: 410
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-938-864-333

RESULT 101
 US-10-195-835-333
 ; Sequence 333, Application US/10195835
 ; Publication No. US20030198622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smilthgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; APPLICANT: Mossman, Sally P.
 ; APPLICANT: Evans, Lawrence S.
 ; APPLICANT: Swanson, Ryan M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C8
 ; CURRENT FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 333
 ; LENGTH: 410
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-195-835-333

Query Match 100.0%; Score 51; DB 11; Length 410;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 51; DB 12; Length 410;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 100
 US-09-785-019-333
 ; Sequence 333, Application US/09785019
 ; Publication No. US20030082196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smilthgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Sleath, Paul
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C4
 ; CURRENT FILING DATE: 2001-02-15
 ; NUMBER OF SEQ ID NOS: 376
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 333
 ; LENGTH: 410
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-785-019-333

RESULT 102
 US-10-286-333-333
 ; Sequence 333, Application US/10286333
 ; Publication No. US20030215458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Jaya, No. US20030215458A1a1e
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C10
 ; CURRENT FILING DATE: 2002-10-30
 ; NUMBER OF SEQ ID NOS: 506
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 333
 ; LENGTH: 410
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-286-333-333

Query Match 100.0%; Score 51; DB 11; Length 410;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 51; DB 11; Length 410;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 103
 US-10-244-830-333
 ; Sequence 333, Application US/10244830
 ; Publication No. US20030235557A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C9
 ; CURRENT FILING DATE: 2002-09-16
 ; CURRENT APPLICATION NUMBER: US/10/244,830
 ; NUMBER OF SEQ ID NOS: 468
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 333
 ; LENGTH: 410
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-244-830-333

Query Match 100.0%; Score 51; DB 12; Length 410;
 Best Local Similarity 100.0%; Pred. No. 0.35;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
 |||||
 Db 287 RMPFNAPYL 295

RESULT 104
 US-10-125-635A-333
 ; Sequence 333, Application US/10125635A
 ; Publication No. US20030039635A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 ; FILE REFERENCE: 210121.465C7
 ; CURRENT APPLICATION NUMBER: US/10/125,635A
 ; CURRENT FILING DATE: 2002-07-19
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 333
 ; LENGTH: 410
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-125-635A-333

Query Match 100.0%; Score 51; DB 15; Length 410;
 Best Local Similarity 100.0%; Pred. No. 0.35;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
 |||||
 Db 287 RMPFNAPYL 295

RESULT 105
 US-10-002-603-333
 ; Sequence 333, Application US/100002603
 ; Publication No. US20030095971A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smithgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedvick, Thomas S.

APPLICANT: Sleath, Paul R.
 APPLICANT: Mossman, Sally
 APPLICANT: Evans, Lawrence
 APPLICANT: Spies, A. Gregory
 APPLICANT: Boydston, Jeremy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C6
 ; CURRENT APPLICATION NUMBER: US/10/002,603
 ; CURRENT FILING DATE: 2001-10-30
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 333
 ; LENGTH: 410
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-002-603-333

Query Match 100.0%; Score 51; DB 15; Length 410;
 Best Local Similarity 100.0%; Pred. No. 0.35;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
 |||||
 Db 287 RMPFNAPYL 295

RESULT 106
 US-09-938-864-393
 ; Sequence 393, Application US/09938864
 ; Publication No. US20030072767A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smithgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Mossman, Sally
 ; APPLICANT: Evans, Lawrence
 ; APPLICANT: Spies, A. Gregory
 ; APPLICANT: Boydston, Jeremy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C5
 ; CURRENT APPLICATION NUMBER: US/09/938,864
 ; CURRENT FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 393
 ; LENGTH: 420
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-938-864-393

Query Match 100.0%; Score 51; DB 11; Length 420;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
 |||||
 Db 265 RMPFNAPYL 273

RESULT 107
 US-10-195-835-393
 ; Sequence 393, Application US/10195835
 ; Publication No. US20030198622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.

```

; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-244-830-393
Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 420;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMFPNAPYL 9
Db 265 RMFPNAPYL 273

```

```

RESULT 108
US-10-286-333-393
; Sequence 393, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Java, No. US20030215458A1a1e
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 393
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-286-333-393

```

```

Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 420;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMFPNAPYL 9
Db 265 RMFPNAPYL 273

```

```

RESULT 109
US-10-244-830-393
; Sequence 393, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244,830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 393
; LENGTH: 420

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-244-830-393
Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 420;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMFPNAPYL 9
Db 265 RMFPNAPYL 273

```

```

RESULT 110
US-10-125-635A-393
; Sequence 393, Application US/10125635A
; Publication No. US2003039635A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Smitbgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 393
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-125-635A-393

```

```

Query Match
Best Local Similarity 100.0%; Score 51; DB 15; Length 420;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMFPNAPYL 9
Db 265 RMFPNAPYL 273

```

```

RESULT 111
US-10-002-603-393
; Sequence 393, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smitbgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 393
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-002-603-393

```

Query Match 100.0%; Score 51; DB 15; Length 420;
 Best Local Similarity 100.0%; Pred. No. 0.36; Mismatches 0;
 Matches 9; Conservative 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
 |||||
 Db 265 RMPFNAPYL 273

RESULT 112
 US-09-938-864-405 Application US/09938864
 ; Sequence 405, Application No. US20030072767A1
 ; Publication No. US20030072767A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Galger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smithgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Mossman, Sally
 ; APPLICANT: Evans, Lawrence
 ; APPLICANT: Spies, A. Gregory
 ; APPLICANT: Boydston, Jeremy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
 ; FILE REFERENCE: 210121.465C5
 ; CURRENT APPLICATION NUMBER: US/09/938, 864
 ; CURRENT FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 405
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-938-864-405

Query Match 100.0%; Score 51; DB 11; Length 428;
 Best Local Similarity 100.0%; Pred. No. 0.37; Mismatches 0;
 Matches 9; Conservative 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
 |||||
 Db 126 RMPFNAPYL 134

RESULT 113
 US-10-195-835-405 Application US/10195835
 ; Sequence 405, Application No. US20030198622A1
 ; Publication No. US20030198622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Galger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; APPLICANT: Mossman, Sally P.
 ; APPLICANT: Swanson, Lawrence S.
 ; APPLICANT: Swanson, Ryan M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
 ; FILE REFERENCE: 210121.465C8
 ; CURRENT APPLICATION NUMBER: US/10/195, 835
 ; CURRENT FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 405
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-195-835-405

Query Match 100.0%; Score 51; DB 12; Length 428;
 Best Local Similarity 100.0%; Pred. No. 0.37; Mismatches 0;
 Matches 9; Conservative 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
 |||||
 Db 126 RMPFNAPYL 134

RESULT 114
 US-10-286-333-405 Application US/10286333
 ; Sequence 405, Application No. US20030215458A1
 ; Publication No. US20030215458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Galger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Java, No. US20030215458A1
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
 ; FILE REFERENCE: 210121.465C10
 ; CURRENT APPLICATION NUMBER: US/10/286, 333
 ; CURRENT FILING DATE: 2002-10-30
 ; NUMBER OF SEQ ID NOS: 506
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 405
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-286-333-405

Query Match 100.0%; Score 51; DB 12; Length 428;
 Best Local Similarity 100.0%; Pred. No. 0.37; Mismatches 0;
 Matches 9; Conservative 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
 |||||
 Db 126 RMPFNAPYL 134

RESULT 115
 US-10-244-830-405 Application US/10244830
 ; Sequence 405, Application No. US20030235557A1
 ; Publication No. US20030235557A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Galger, Alexander
 ; APPLICANT: Cheever, Martin A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
 ; FILE REFERENCE: 210121.465C9
 ; CURRENT APPLICATION NUMBER: US/10/244, 830
 ; CURRENT FILING DATE: 2002-09-16
 ; NUMBER OF SEQ ID NOS: 468
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 405
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-244-830-405

Query Match 100.0%; Score 51; DB 12; Length 428;
 Best Local Similarity 100.0%; Pred. No. 0.37; Mismatches 0;
 Matches 9; Conservative 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
 |||||
 Db 126 RMPFNAPYL 134

RESULT 116
 US-10-125-635A-405 Application US/10125635A
 ; Sequence 405, Application No. US2003039635A1
 ; Publication No. US2003039635A1

```

: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: Smithgall, Molly D.
: APPLICANT: Carter, Darrick
: APPLICANT: Cheever, Martin A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Sutherland, R. Alec
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
: TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465C7
: CURRENT APPLICATION NUMBER: US/10/125,635A
: CURRENT FILING DATE: 2002-07-19
: NUMBER OF SEQ ID NOS: 461
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 405
: LENGTH: 428
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-125-635A-405

```

```

Query Match          100.0%; Score 51; DB 15; Length 428;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 117
US-10-002-603-405
: Sequence 405, Application US/10002603
: Publication No. US20030095977A1
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Smithgall, Molly
: APPLICANT: Moulton, Gus
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Sleath, Paul R.
: APPLICANT: Mossman, Sally
: APPLICANT: Evans, Lawrence
: APPLICANT: Spies, A. Gregory
: APPLICANT: Boydston, Jeremy
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
: TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465C6
: CURRENT APPLICATION NUMBER: US/10/002,603
: CURRENT FILING DATE: 2001-10-30
: NUMBER OF SEQ ID NOS: 413
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 405
: LENGTH: 428
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-002-603-405

```

```

Query Match          100.0%; Score 51; DB 15; Length 428;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 118
US-09-938-864-408
: Sequence 408, Application US/09938864
: Publication No. US200300767A1
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: McNeill, Patricia D.

```

```

: APPLICANT: Smithgall, Molly
: APPLICANT: Moulton, Gus
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Sleath, Paul R.
: APPLICANT: Mossman, Sally
: APPLICANT: Evans, Lawrence
: APPLICANT: Spies, A. Gregory
: APPLICANT: Boydston, Jeremy
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
: TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465C5
: CURRENT APPLICATION NUMBER: US/09/938,864
: CURRENT FILING DATE: 2001-08-24
: NUMBER OF SEQ ID NOS: 413
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 408
: LENGTH: 429
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-938-864-408

```

```

Query Match          100.0%; Score 51; DB 11; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 119
US-10-195-835-408
: Sequence 408, Application US/10195835
: Publication No. US20030198622A1
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: Smithgall, Molly D.
: APPLICANT: Carter, Darrick
: APPLICANT: Cheever, Martin A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Sutherland, R. Alec
: APPLICANT: Mossman, Sally P.
: APPLICANT: Evans, Lawrence S.
: APPLICANT: Swanson, Ryan M.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
: TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465C8
: CURRENT APPLICATION NUMBER: US/10/195,835
: CURRENT FILING DATE: 2002-07-12
: NUMBER OF SEQ ID NOS: 461
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 408
: LENGTH: 429
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-195-835-408

```

```

Query Match          100.0%; Score 51; DB 12; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 120
US-10-286-333-408
: Sequence 408, Application US/10286333
: Publication No. US20030215458A1
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: McNeill, Patricia D.

```

```

; ORGANISM: Homo sapiens
; US-10-125-635A-408
Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 429;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

; ORGANISM: Homo sapiens
; US-10-244-830-408
Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 429;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

RESULT 121
; Sequence 408, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244,830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 408
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-244-830-408
Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 429;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

; ORGANISM: Homo sapiens
; US-10-125-635A-408
Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 429;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

; ORGANISM: Homo sapiens
; US-10-002-603-408
Query Match
Best Local Similarity 100.0%; Score 51; DB 15; Length 429;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

; ORGANISM: Homo sapiens
; US-10-002-603-408
Query Match
Best Local Similarity 100.0%; Score 51; DB 15; Length 429;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

RESULT 123
; Sequence 408, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 408
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-002-603-408
Query Match
Best Local Similarity 100.0%; Score 51; DB 15; Length 429;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

; ORGANISM: Homo sapiens
; US-09-929-315-4
Query Match
Best Local Similarity 100.0%; Score 51; DB 15; Length 429;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

; ORGANISM: Homo sapiens
; US-09-929-315-4
Query Match
Best Local Similarity 100.0%; Score 51; DB 15; Length 429;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

PRIOR APPLICATION NUMBER: US 07/614,161
PRIOR FILING DATE: 1990-11-13
PRIOR APPLICATION NUMBER: US 07/435,780
PRIOR FILING DATE: 1989-11-13
PRIOR APPLICATION NUMBER: US 07/795,323
PRIOR FILING DATE: 1991-11-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 449
TYPE: PRT
ORGANISM: Unknown
FEATURES:
OTHER INFORMATION: Murine
US-09-929-315-4

```

```

Query Match 100.0%; Score 51; DB 9; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 125
US-09-929-315-6
Sequence 6, Application US/09929315
Patent No. US20020082394A1
GENERAL INFORMATION:
APPLICANT: Call, Katherine M.
APPLICANT: Glaser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Housman, David E.
APPLICANT: Bruening, Wendy
TITLE OF INVENTION: Localization and Characterization of the
FILE REFERENCE: 0050.1312-013
CURRENT APPLICATION NUMBER: US/09/929,315
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 09/037,179
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 08/102,942
PRIOR FILING DATE: 1993-08-02
PRIOR APPLICATION NUMBER: US 07/614,161
PRIOR FILING DATE: 1990-11-13
PRIOR APPLICATION NUMBER: US 07/435,780
PRIOR FILING DATE: 1989-11-13
PRIOR APPLICATION NUMBER: US 07/795,323
PRIOR FILING DATE: 1991-11-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 449
TYPE: PRT
ORGANISM: Homo sapien
US-09-929-315-6

```

```

Query Match 100.0%; Score 51; DB 9; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

RESULT 126

```

US-09-993-215-4
Sequence 4, Application US/09993215
Patent No. US20020128196A1
GENERAL INFORMATION:
APPLICANT: Call, Katherine M.
APPLICANT: Glaser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Housman, David E.
APPLICANT: Bruening, Wendy
APPLICANT: Darveau, Andre
TITLE OF INVENTION: Localization and Characterization of the
FILE REFERENCE: 0050.1312-014
CURRENT APPLICATION NUMBER: US/09/993,215
PRIOR FILING DATE: 2001-11-12
PRIOR APPLICATION NUMBER: US 09/037,179
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 08/102,942
PRIOR FILING DATE: 1993-08-02
PRIOR APPLICATION NUMBER: US 07/614,161
PRIOR FILING DATE: 1990-11-13
PRIOR APPLICATION NUMBER: US 07/435,780
PRIOR FILING DATE: 1989-11-13
PRIOR APPLICATION NUMBER: US 07/795,323
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 449
TYPE: PRT
ORGANISM: Unknown
FEATURES:
OTHER INFORMATION: Murine
US-09-993-215-4

```

```

Query Match 100.0%; Score 51; DB 10; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 127
US-09-993-215-6
Sequence 6, Application US/09993215
Patent No. US20020128196A1
GENERAL INFORMATION:
APPLICANT: Call, Katherine M.
APPLICANT: Glaser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Housman, David E.
APPLICANT: Bruening, Wendy
APPLICANT: Darveau, Andre
TITLE OF INVENTION: Localization and Characterization of the
FILE REFERENCE: 0050.1312-014
CURRENT APPLICATION NUMBER: US/09/993,215
PRIOR FILING DATE: 2001-11-12
PRIOR APPLICATION NUMBER: US 09/037,179
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 08/102,942
PRIOR FILING DATE: 1993-08-02
PRIOR APPLICATION NUMBER: US 07/614,161

```

```

PRIOR FILING DATE: 1990-11-13
PRIOR APPLICATION NUMBER: US 07/435,780
PRIOR FILING DATE: 1989-11-13
PRIOR APPLICATION NUMBER: US 07/795,323
PRIOR FILING DATE: 1991-11-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 6
LENGTH: 449
TYPE: PRT
ORGANISM: Homo sapien
US-09-938-215-6

```

```

Query Match      100.0%; Score 51; DB 10; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 128
US-09-938-864-319
Sequence 319, Application US/09938864
Publication No. US20030072767A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: McNeill, Patricia D.
APPLICANT: Smithgall, Molly
APPLICANT: Moulton, Gus
APPLICANT: Vedvick, Thomas S.
APPLICANT: Sleath, Paul R.
APPLICANT: Mossman, Sally
APPLICANT: Evans, Lawrence
APPLICANT: Spies, A. Gregory
APPLICANT: Boydston, Jeremy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
FILE REFERENCE: 210121.465C5
CURRENT APPLICATION NUMBER: US/09/938,864
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 413
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 319
LENGTH: 449
TYPE: PRT
ORGANISM: Homo sapien
US-09-938-864-319

```

```

Query Match      100.0%; Score 51; DB 11; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 129
US-09-938-864-320
Sequence 320, Application US/09938864
Publication No. US20030072767A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: McNeill, Patricia D.
APPLICANT: Smithgall, Molly
APPLICANT: Moulton, Gus
APPLICANT: Vedvick, Thomas S.
APPLICANT: Sleath, Paul R.
APPLICANT: Mossman, Sally
APPLICANT: Evans, Lawrence
APPLICANT: Spies, A. Gregory

```

```

APPLICANT: Boydston, Jeremy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
FILE REFERENCE: 210121.465C5
CURRENT APPLICATION NUMBER: US/09/938,864
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 413
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 320
LENGTH: 449
TYPE: PRT
ORGANISM: Mus musculus
US-09-938-864-320

```

```

Query Match      100.0%; Score 51; DB 11; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 130
US-09-938-864-404
Sequence 404, Application US/09938864
Publication No. US20030072767A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: McNeill, Patricia D.
APPLICANT: Smithgall, Molly
APPLICANT: Moulton, Gus
APPLICANT: Vedvick, Thomas S.
APPLICANT: Sleath, Paul R.
APPLICANT: Mossman, Sally
APPLICANT: Evans, Lawrence
APPLICANT: Spies, A. Gregory
APPLICANT: Boydston, Jeremy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
FILE REFERENCE: 210121.465C5
CURRENT APPLICATION NUMBER: US/09/938,864
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 413
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 404
LENGTH: 449
TYPE: PRT
ORGANISM: Homo sapiens
US-09-938-864-404

```

```

Query Match      100.0%; Score 51; DB 11; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 131
US-09-791-477-319
Sequence 319, Application US/09791477
Publication No. US20030082194A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Cheever, Martin A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
FILE REFERENCE: 2077.000200
CURRENT APPLICATION NUMBER: US/09/791,477
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/184,070

```

PRIOR FILING DATE: 2000-02-22
 : NUMBR OF SEQ ID NOS: 326
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 319
 : LENGTH: 449
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 US-09-791-477-319

Query Match 100.0%; Score 51; DB 11; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
 |||||
 Db 126 RMPFNAPYL 134

RESULT 132
 US-09-791-477-320
 : Sequence 320, Application US/09791477
 : Publication No. US20030082194A1
 : GENERAL INFORMATION:
 : APPLICANT: Gaiger, Alexander
 : APPLICANT: Cheever, Martin A.
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
 : TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
 : FILE REFERENCE: 2077.000200
 : CURRENT APPLICATION NUMBER: US/09/791,477
 : CURRENT FILING DATE: 2001-02-22
 : PRIOR APPLICATION NUMBER: 60/184,070
 : PRIOR FILING DATE: 2000-02-22
 : NUMBER OF SEQ ID NOS: 326
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 320
 : LENGTH: 449
 : TYPE: PRT
 : ORGANISM: Mus musculus
 US-09-791-477-320

Query Match 100.0%; Score 51; DB 11; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
 |||||
 Db 126 RMPFNAPYL 134

RESULT 133
 US-09-785-019-319
 : Sequence 319, Application US/09785019
 : Publication No. US20030082196A1
 : GENERAL INFORMATION:
 : APPLICANT: Gaiger, Alexander
 : APPLICANT: Cheever, Martin A.
 : APPLICANT: McNeill, Patricia D.
 : APPLICANT: Smithgall, Molly
 : APPLICANT: Moulton, Gus
 : APPLICANT: Vedvick, Thomas S.
 : APPLICANT: Sleath, Paul
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 : TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 : FILE REFERENCE: 210121.465C4
 : CURRENT APPLICATION NUMBER: US/09/785,019
 : CURRENT FILING DATE: 2001-02-15
 : NUMBER OF SEQ ID NOS: 376
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 319
 : LENGTH: 449
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 US-09-785-019-319

Query Match 100.0%; Score 51; DB 11; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
 |||||
 Db 126 RMPFNAPYL 134

RESULT 134
 US-09-785-019-320
 : Sequence 320, Application US/09785019
 : Publication No. US20030082196A1
 : GENERAL INFORMATION:
 : APPLICANT: Gaiger, Alexander
 : APPLICANT: Cheever, Martin A.
 : APPLICANT: McNeill, Patricia D.
 : APPLICANT: Smithgall, Molly
 : APPLICANT: Moulton, Gus
 : APPLICANT: Vedvick, Thomas S.
 : APPLICANT: Sleath, Paul
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 : TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 : FILE REFERENCE: 210121.465C4
 : CURRENT APPLICATION NUMBER: US/09/785,019
 : CURRENT FILING DATE: 2001-02-15
 : NUMBER OF SEQ ID NOS: 376
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 320
 : LENGTH: 449
 : TYPE: PRT
 : ORGANISM: Mus musculus
 US-09-785-019-320

Query Match 100.0%; Score 51; DB 11; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
 |||||
 Db 126 RMPFNAPYL 134

RESULT 135
 US-10-177-390-4
 : Sequence 4, Application US/10177390
 : Publication No. US20030143743A1
 : GENERAL INFORMATION:
 : APPLICANT: Schuler, Gerold
 : APPLICANT: N.V. Antwerp Innovatiecentrum
 : TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with Linear
 : TITLE OF INVENTION: Polynucleotides by Electroporation
 : FILE REFERENCE: 021505wc/JH/ml
 : CURRENT APPLICATION NUMBER: US/10/177,390
 : CURRENT FILING DATE: 2002-06-20
 : NUMBER OF SEQ ID NOS: 34
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 4
 : LENGTH: 449
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 US-10-177-390-4

Query Match 100.0%; Score 51; DB 12; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
 |||||
 Db 126 RMPFNAPYL 134

RESULT 136
 US-10-195-835-319
 ; Sequence 319, Application US/10195835
 ; Publication No. US20030198622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; APPLICANT: Mossman, Sally P.
 ; APPLICANT: Evans, Lawrence S.
 ; APPLICANT: Swanson, Ryan M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C8
 ; CURRENT APPLICATION NUMBER: US/10/195,835
 ; CURRENT FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 319
 ; LENGTH: 449
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-195-835-319

Query Match 100.0%; Score 51; DB 12; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 Db 126 RMPFNAPYL 134

RESULT 137
 US-10-195-835-320
 ; Sequence 320, Application US/10195835
 ; Publication No. US20030198622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; APPLICANT: Mossman, Sally P.
 ; APPLICANT: Evans, Lawrence S.
 ; APPLICANT: Swanson, Ryan M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C8
 ; CURRENT APPLICATION NUMBER: US/10/195,835
 ; CURRENT FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 320
 ; LENGTH: 449
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-195-835-320

Query Match 100.0%; Score 51; DB 12; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 Db 126 RMPFNAPYL 134

RESULT 138

US-10-195-835-404
 ; Sequence 404, Application US/10195835
 ; Publication No. US20030198622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; APPLICANT: Mossman, Sally P.
 ; APPLICANT: Evans, Lawrence S.
 ; APPLICANT: Swanson, Ryan M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C8
 ; CURRENT APPLICATION NUMBER: US/10/195,835
 ; CURRENT FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 404
 ; LENGTH: 449
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-195-835-404

Query Match 100.0%; Score 51; DB 12; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 Db 126 RMPFNAPYL 134

RESULT 139
 US-10-286-333-319
 ; Sequence 319, Application US/10286333
 ; Publication No. US20030215458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Jaya, No. US20030215458A1a1e
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C10
 ; CURRENT APPLICATION NUMBER: US/10/286,333
 ; CURRENT FILING DATE: 2002-10-30
 ; NUMBER OF SEQ ID NOS: 506
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 319
 ; LENGTH: 449
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-286-333-319

Query Match 100.0%; Score 51; DB 12; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 Db 126 RMPFNAPYL 134

RESULT 140
 US-10-286-333-320
 ; Sequence 320, Application US/10286333
 ; Publication No. US20030215458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Jaya, No. US20030215458A1a1e

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286.333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 320
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-286-333-320

```

```

Query Match          100.0%; Score 51; DB 12; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
    |||||
Db 126 RMPFNAPYL 134

```

```

RESULT 141
US-10-286-333-404 Application US/10286333
; Sequence 404, Application No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Java, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286.333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 404
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-404

```

```

Query Match          100.0%; Score 51; DB 12; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
    |||||
Db 126 RMPFNAPYL 134

```

```

RESULT 142
US-10-244-830-319 Application US/10244830
; Sequence 319, Application No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244.830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 319
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-244-830-319

```

```

Query Match          100.0%; Score 51; DB 12; Length 449;

```

```

Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
    |||||
Db 126 RMPFNAPYL 134

```

```

RESULT 143
US-10-244-830-320 Application US/10244830
; Sequence 320, Application No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244.830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 320
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-244-830-320

```

```

Query Match          100.0%; Score 51; DB 12; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
    |||||
Db 126 RMPFNAPYL 134

```

```

RESULT 144
US-10-244-830-404 Application US/10244830
; Sequence 404, Application No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244.830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 404
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-244-830-404

```

```

Query Match          100.0%; Score 51; DB 12; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 RMPFNAPYL 9
    |||||
Db 126 RMPFNAPYL 134

```

```

RESULT 145
US-10-125-635A-319 Application US/10125635A
; Sequence 319, Application No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Smithgall, Molly D.
US-10-125-635A-319

```

```

Query Match          100.0%; Score 51; DB 12; Length 449;

```

```

; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125.635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-125-635A-319

```

```

Query Match 100.0%; Score 51; DB 15; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 146
US-10-125-635A-320
; Sequence 320, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125.635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 320
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-125-635A-320

```

```

Query Match 100.0%; Score 51; DB 15; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 147
US-10-125-635A-404
; Sequence 404, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7

```

```

; CURRENT APPLICATION NUMBER: US/10/125.635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 404
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-404

```

```

Query Match 100.0%; Score 51; DB 15; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 148
US-10-002-603-319
; Sequence 319, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Patricia D.
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002.603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-002-603-319

```

```

Query Match 100.0%; Score 51; DB 15; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 149
US-10-002-603-320
; Sequence 320, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7

```

```

; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 320
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-002-603-320

```

```

Query Match          100.0%; Score 51; DB 15; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        126 RMPFNAPYL 134

```

```

RESULT 150
US-10-002-603-404
; Sequence 404, Application US/10002603
; Publication No. US20030095971A1
GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithegall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 404
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-603-404

```

```

Query Match          100.0%; Score 51; DB 15; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        126 RMPFNAPYL 134

```

```

Search completed: January 21, 2004, 09:11:50
Job time : 34 secs

```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 21, 2004, 08:42:29 ; Search time 22 Seconds
(Without alignments)
17.309 Million cell updates/sec

Title: US-09-625-963A-1

Perfect score: 51

Sequence: 1 RMEFNPARYL 9

Scoring table: BIOSDM62
Gapop 10.0 0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

- 1: Issued Patents AA:*
- 2: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	154	1 US-08-102-942A-5	Sequence 5, Appli
2	51	100.0	154	4 US-09-037-179B-5	Sequence 5, Appli
3	51	100.0	210	1 US-08-234-783-2	Sequence 2, Appli
4	51	100.0	210	1 US-08-456-907-2	Sequence 2, Appli
5	51	100.0	210	5 PCT-US95-05523-2	Sequence 2, Appli
6	51	100.0	345	1 US-08-102-942A-2	Sequence 2, Appli
7	51	100.0	345	4 US-09-037-179B-2	Sequence 2, Appli
8	51	100.0	429	1 US-08-234-783-4	Sequence 4, Appli
9	51	100.0	429	1 US-08-456-907-4	Sequence 4, Appli
10	51	100.0	429	5 PCT-US95-05523-4	Sequence 4, Appli
11	51	100.0	449	1 US-08-102-942A-4	Sequence 4, Appli
12	51	100.0	449	1 US-08-102-942A-6	Sequence 4, Appli
13	51	100.0	449	1 US-09-037-179B-4	Sequence 4, Appli
14	51	100.0	449	4 US-09-037-179B-6	Sequence 4, Appli
15	38	74.5	269	4 US-09-252-991A-19580	Sequence 19580, A
16	37	72.5	50	3 US-08-975-080-26	Sequence 26, Appli
17	37	72.5	56	4 US-08-657-759-24	Sequence 24, Appli
18	37	72.5	204	4 US-09-134-001C-2975	Sequence 2975, Ap
19	37	72.5	1151	3 US-08-836-134-23	Sequence 23, Appli
20	37	72.5	1151	4 US-09-493-784-23	Sequence 23, Appli
21	21	72.5	1232	3 US-08-836-134-2	Sequence 2, Appli
22	37	72.5	1232	4 US-09-493-784-2	Sequence 2, Appli
23	36	70.6	67	2 US-08-511-485-23	Sequence 23, Appli
24	36	70.6	67	4 US-09-201-936-23	Sequence 23, Appli
25	36	70.6	217	3 US-08-297-431B-33	Sequence 33, Appli
26	36	70.6	365	4 US-09-818-512-4	Sequence 4, Appli
27	36	70.6	370	3 US-09-150-133-1	Sequence 1, Appli

Result No.	Score	Query Match	Length	DB ID	Description
28	36	70.6	370	3 US-09-150-133-3	Sequence 3, Appli
29	36	70.6	370	3 US-09-150-141-1	Sequence 1, Appli
30	36	70.6	370	3 US-09-150-141-3	Sequence 1, Appli
31	36	70.6	370	3 US-09-374-493-1	Sequence 1, Appli
32	36	70.6	370	3 US-09-374-493-3	Sequence 3, Appli
33	36	70.6	370	3 US-09-374-824-1	Sequence 1, Appli
34	36	70.6	370	3 US-09-374-824-3	Sequence 3, Appli
35	36	70.6	370	3 US-09-374-492-1	Sequence 1, Appli
36	36	70.6	370	3 US-09-374-492-3	Sequence 3, Appli
37	36	70.6	370	4 US-09-849-562A-2	Sequence 2, Appli
38	36	70.6	370	4 US-09-849-031A-2	Sequence 2, Appli
39	36	70.6	376	4 US-09-818-512-2	Sequence 2, Appli
40	36	70.6	389	3 US-08-430-286A-7	Sequence 7, Appli
41	36	70.6	438	5 PCT-US95-05923A-2	Sequence 2, Appli
42	36	70.6	618	2 US-08-511-485-8	Sequence 8, Appli
43	36	70.6	618	3 US-09-212-971-8	Sequence 8, Appli
44	36	70.6	618	3 US-08-800-929A-8	Sequence 8, Appli
45	36	70.6	618	3 US-08-569-749-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-102-942A-5

Sequence 5, Application US/08102942A
Patent No. 5726288

GENERAL INFORMATION:

APPLICANT: Calli, Katherine M.

APPLICANT: Glaeser, Thomas M.

APPLICANT: Ito, Caryn Y.

APPLICANT: Buckler, Alan J.

APPLICANT: Bellefleur, Jerry

APPLICANT: Haber, Daniel A.

APPLICANT: Rose, Blise A.

APPLICANT: Housman, David E.

APPLICANT: Bruening, Wendy

APPLICANT: Daryeau, Andre

TITLE OF INVENTION: Localization and Characterization of the

TITLE OF INVENTION: Wilms' Tumor Gene

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: U.S.

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/102,942A

FILING DATE: 02-AUG-1993

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: MIT-5194A2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEPHONE: 617-861-9540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 154 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-102-942A-5

Query Match 100.0%; Score 51; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 40 RMPFNAPYL 48

RESULT 2

US-09-037-179B-5
 ; Sequence 5, Application US/09037179B
 ; Patent No. 6316599
 ; GENERAL INFORMATION:
 ; APPLICANT: Call, Katherine M.
 ; APPLICANT: Glaser, Thomas M.
 ; APPLICANT: Ito, Caryn Y.
 ; APPLICANT: Buckler, Alan J.
 ; APPLICANT: Pelletier, Jerry
 ; APPLICANT: Haber, Daniel A.
 ; APPLICANT: Rose, Elise A.
 ; APPLICANT: Housman, David E.
 ; APPLICANT: Brunsing, Wendy
 ; APPLICANT: Darveau, Andre
 ; TITLE OF INVENTION: Localization and Characterization of the
 ; TITLE OF INVENTION: Wilms' Tumor Gene
 ; FILE REFERENCE: 0050.1312-011
 ; CURRENT APPLICATION NUMBER: US/09/037.179B
 ; CURRENT FILING DATE: 1998-03-09
 ; PRIOR APPLICATION NUMBER: US 08/102,942
 ; PRIOR FILING DATE: 1993-08-02
 ; PRIOR APPLICATION NUMBER: US 07/614,161
 ; PRIOR FILING DATE: 1990-11-13
 ; PRIOR APPLICATION NUMBER: US 07/435,780
 ; PRIOR FILING DATE: 1989-11-13
 ; PRIOR APPLICATION NUMBER: US 07/795,323
 ; PRIOR FILING DATE: 1994-09-27
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 154
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-037-179B-5

Query Match 100.0%; Score 51; DB 4; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 40 RMPFNAPYL 48

RESULT 3
 ; US-08-234-783-2
 ; Sequence 2, Application US/08234783
 ; Patent No. 5622835
 ; GENERAL INFORMATION:
 ; APPLICANT: Herlyn, Meenhard
 ; APPLICANT: Morris, Jennifer
 ; APPLICANT: Rauscher III, Frank J.
 ; APPLICANT: Rodeck, Ulrich
 ; TITLE OF INVENTION: W1 Monoclonal Antibodies and Methods of
 ; TITLE OF INVENTION: Use Therefor
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howson and Howson
 ; STREET: Spring House Corporate Cntr, PO Box 457
 ; CITY: Spring House
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19477

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/234,783
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Bak, Mary E.
 REGISTRATION NUMBER: 31,215
 REFERENCE/DOCKET NUMBER: WST48USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-540-9200
 TELEFAX: 215-540-5818
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 210 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-234-783-2

Query Match 100.0%; Score 51; DB 1; Length 210;
 Best Local Similarity 100.0%; Pred. No. 0.071;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9
 |||||
 Db 137 RMPFNAPYL 145

RESULT 4

US-08-456-907-2
 ; Sequence 2, Application US/08456907
 ; Patent No. 5633142
 ; GENERAL INFORMATION:
 ; APPLICANT: Herlyn, Meenhard
 ; APPLICANT: Morris, Jennifer
 ; APPLICANT: Rauscher III, Frank J.
 ; APPLICANT: Rodeck, Ulrich
 ; TITLE OF INVENTION: W1 Monoclonal Antibodies and Methods of
 ; TITLE OF INVENTION: Use Therefor
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howson and Howson
 ; STREET: Spring House Corporate Cntr, PO Box 457
 ; CITY: Spring House
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19477
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/456,907
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/234,783
 ; FILING DATE: 28-APR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bak, Mary E.
 ; REGISTRATION NUMBER: 31,215
 ; REFERENCE/DOCKET NUMBER: WST48AUSA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-540-9200
 ; TELEFAX: 215-540-5818
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 210 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-907-2

Query Match 100.0%; Score 51; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
Db 137 RMPFNAPYL 145

RESULT 5
PCT-US95-05523-2 Application PC/TUS9505523

GENERAL INFORMATION:
APPLICANT: The Wistar Institute of Anatomy and Biology
TITLE OF INVENTION: WTI Monoclonal Antibodies and
METHODS OF USE Therefor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,783
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Marty E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST48PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-05523-2

Query Match 100.0%; Score 51; DB 5; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
Db 137 RMPFNAPYL 145

RESULT 6
US-08-102-942A-2
Sequence 2, Application US/08102942A
Patent No. 5726288
GENERAL INFORMATION:
APPLICANT: Calli, Katherine M.
APPLICANT: Glaeser, Thomas M.

APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Housman, David E.
APPLICANT: Bruening, Wendy
APPLICANT: Darveau, Andre
TITLE OF INVENTION: Localization and Characterization of the
TITLE OF INVENTION: Wilms' Tumor Gene
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,942A
FILING DATE: 02-AUG-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5194A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-102-942A-2

Query Match 100.0%; Score 51; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
Db 42 RMPFNAPYL 50

RESULT 7
US-09-037-179B-2 Application US/09037179B
Patent No. 6315599
GENERAL INFORMATION:
APPLICANT: Calli, Katherine M.
APPLICANT: Glaeser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Housman, David E.
APPLICANT: Bruening, Wendy
APPLICANT: Darveau, Andre
TITLE OF INVENTION: Localization and Characterization of the
TITLE OF INVENTION: Wilms' Tumor Gene
FILE REFERENCE: 0050,1312-011
CURRENT APPLICATION NUMBER: US/09/037,179B
CURRENT FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 08/102,942
PRIOR FILING DATE: 1993-08-02

```

PRIOR APPLICATION NUMBER: US 07/614,161
PRIOR FILING DATE: 1990-11-13
PRIOR APPLICATION NUMBER: US 07/435,780
PRIOR FILING DATE: 1989-11-13
PRIOR APPLICATION NUMBER: US 07/795,323
PRIOR FILING DATE: 1994-09-27
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapien
US-09-037-179B-2

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```

Query Match 100.0%; Score 51; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 RMPFNAPYL 9
Db 42 RMPFNAPYL 50

```

```

RESULT 8
US-08-234-783-4
Sequence 4, Application US/08234783
Patent No. 5622835
GENERAL INFORMATION:
APPLICANT: Herlyn, Meenhard
APPLICANT: Morris, Jennifer
APPLICANT: Rauscher III, Frank J.
APPLICANT: Rodeck, Ulrich
TITLE OF INVENTION: Wtl Monoclonal Antibodies and Methods of
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,783
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST48AUSA
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-234-783-4

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```

RESULT 9
US-08-456-907-4
Sequence 4, Application US/08456907
Patent No. 5633142
GENERAL INFORMATION:
APPLICANT: Herlyn, Meenhard
APPLICANT: Morris, Jennifer
APPLICANT: Rauscher III, Frank J.
APPLICANT: Rodeck, Ulrich
TITLE OF INVENTION: Wtl Monoclonal Antibodies and Methods of
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,907
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,783
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST48AUSA
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-907-4

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```

Query Match 100.0%; Score 51; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134

```

```

RESULT 10
PCT-US95-05523-4
Sequence 4, Application PC/TUS9505523
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of Anatomy and Biology
TITLE OF INVENTION: Wtl Monoclonal Antibodies and
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05523
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/234,783
 FILING DATE: 28-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bak, Mary E.
 REGISTRATION NUMBER: 31,215
 REFERENCE/DOCKET NUMBER: MST48PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-540-9200
 TELEFAX: 215-540-5818
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 429 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-05523-4

Query Match 100.0%; Score 51; DB 5; Length 429;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPNAPYL 9
 Db 126 RMPNAPYL 134

RESULT 11
 US-08-102-942A-4
 Sequence 4, Application US/08102942A
 Patent No. 5726288
 GENERAL INFORMATION:
 APPLICANT: Call, Katherine M.
 APPLICANT: Glaser, Thomas M.
 APPLICANT: Ito, Caryn Y.
 APPLICANT: Buckler, Alan J.
 APPLICANT: Pelletier, Jerry
 APPLICANT: Haber, Daniel A.
 APPLICANT: Rose, Elise A.
 APPLICANT: Housman, David E.
 APPLICANT: Bruening, Wendy
 APPLICANT: Darveau, Andre
 TITLE OF INVENTION: Localization and Characterization of the
 TITLE OF INVENTION: Wilms' Tumor Gene
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Millitia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: U.S.
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/102,942A
 FILING DATE: 02-AUG-1993
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: MIT-5194A2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 449 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-102-942A-6

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 449 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-102-942A-4

Query Match 100.0%; Score 51; DB 1; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPNAPYL 9
 Db 126 RMPNAPYL 134

RESULT 12
 US-08-102-942A-6
 Sequence 6, Application US/08102942A
 Patent No. 5726288
 GENERAL INFORMATION:
 APPLICANT: Call, Katherine M.
 APPLICANT: Glaser, Thomas M.
 APPLICANT: Ito, Caryn Y.
 APPLICANT: Buckler, Alan J.
 APPLICANT: Pelletier, Jerry
 APPLICANT: Haber, Daniel A.
 APPLICANT: Rose, Elise A.
 APPLICANT: Housman, David E.
 APPLICANT: Bruening, Wendy
 APPLICANT: Darveau, Andre
 TITLE OF INVENTION: Localization and Characterization of the
 TITLE OF INVENTION: Wilms' Tumor Gene
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Millitia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: U.S.
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/102,942A
 FILING DATE: 02-AUG-1993
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: MIT-5194A2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 449 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-102-942A-6

OY 1 RMPFNAPYL 9
 DB 126 RMPFNAPYL 134

RESULT 13
 US-09-037-179B-4
 ; Sequence 4, Application US/09037179B
 ; Patent No. 6316599
 ; GENERAL INFORMATION:
 ; APPLICANT: Call, Katherine M.
 ; APPLICANT: Glaser, Thomas M.
 ; APPLICANT: Ito, Caryn Y.
 ; APPLICANT: Buckler, Alan J.
 ; APPLICANT: Pelletier, Jerry
 ; APPLICANT: Haber, Daniel A.
 ; APPLICANT: Rose, Elise A.
 ; APPLICANT: Housman, David E.
 ; APPLICANT: Brunsing, Wendy
 ; APPLICANT: Darveau, Andre
 ; TITLE OF INVENTION: Localization and Characterization of the
 ; FILE REFERENCE: 0050.1312-011
 ; CURRENT APPLICATION NUMBER: US/09/037,179B
 ; CURRENT FILING DATE: 1998-03-09
 ; PRIOR APPLICATION NUMBER: US 08/102,942
 ; PRIOR FILING DATE: 1995-08-02
 ; PRIOR APPLICATION NUMBER: US 07/614,161
 ; PRIOR FILING DATE: 1990-11-13
 ; PRIOR APPLICATION NUMBER: US 07/435,780
 ; PRIOR FILING DATE: 1989-11-13
 ; PRIOR APPLICATION NUMBER: US 07/795,323
 ; PRIOR FILING DATE: 1994-09-27
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 449
 ; TYPE: PRT
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Murine
 ; US-09-037-179B-4

Query Match 100.0%; Score 51; DB 4; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
 DB 126 RMPFNAPYL 134

RESULT 14
 US-09-037-179B-6
 ; Sequence 6, Application US/09037179B
 ; Patent No. 6316599
 ; GENERAL INFORMATION:
 ; APPLICANT: Call, Katherine M.
 ; APPLICANT: Glaser, Thomas M.
 ; APPLICANT: Ito, Caryn Y.
 ; APPLICANT: Buckler, Alan J.
 ; APPLICANT: Pelletier, Jerry
 ; APPLICANT: Haber, Daniel A.
 ; APPLICANT: Rose, Elise A.
 ; APPLICANT: Housman, David E.
 ; APPLICANT: Brunsing, Wendy
 ; APPLICANT: Darveau, Andre
 ; TITLE OF INVENTION: Localization and Characterization of the
 ; FILE REFERENCE: 0050.1312-011
 ; CURRENT APPLICATION NUMBER: US/09/037,179B
 ; CURRENT FILING DATE: 1998-03-09

PRIOR APPLICATION NUMBER: US 08/102,942
 ; PRIOR FILING DATE: 1993-08-02
 ; PRIOR APPLICATION NUMBER: US 07/614,161
 ; PRIOR FILING DATE: 1990-11-13
 ; PRIOR APPLICATION NUMBER: US 07/435,780
 ; PRIOR FILING DATE: 1989-11-13
 ; PRIOR APPLICATION NUMBER: US 07/795,323
 ; PRIOR FILING DATE: 1994-09-27
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 449
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-037-179B-6

Query Match 100.0%; Score 51; DB 4; Length 449;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9
 DB 126 RMPFNAPYL 134

RESULT 15
 US-09-252-991A-19580
 ; Sequence 1980, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 19580
 ; LENGTH: 269
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-19580

Query Match 74.5%; Score 38; DB 4; Length 269;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MFPNAPYL 9
 DB 139 MFPNAPYL 146

Search completed: January 21, 2004, 08:45:42
 Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 21, 2004, 08:49:30 ; Search time 20 Seconds
(without alignments)
43.276 Million cell updates/sec

Title: US-09-625-963A-1
Perfect score: 51
Sequence: 1 RMPFNAPYL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 789

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	37.3	9	2	S70345 amine oxidase (cop
2	18	35.3	7	2	D48186 ATPase R1 subunit
3	17	33.3	9	2	PH1408 Ig heavy chain V r
4	17	33.3	9	2	JS0302 xenopsin-related p
5	17	33.3	9	2	AE0320 xenopsin-related p
6	17	33.3	9	2	PI0139 carbon-monoxide de
7	16	31.4	7	2	S21230 dermatophin (Trp-4,
8	16	31.4	8	2	I57018 gene Cfr protein
9	16	31.4	9	2	A44787 calliEMRFamide 4 -
10	16	31.4	9	2	D41978 calliEMRFamide 4 -
11	15	29.4	6	4	S15596 orf 3 rara 5'-regi
12	15	29.4	9	2	S66607 quinoline 2-oxidat
13	15	29.4	9	2	A61620 locustamyotropin I
14	15	29.4	9	2	PH1591 Ig H chain V-D-J r
15	14	27.5	5	2	JS0319 subesophagal gang
16	14	27.5	8	2	S21288 lectin - poraco (F
17	14	27.5	8	2	PT0030 inulinase (EC 3.2.
18	14	27.5	8	2	D47393 inulinase (EC 3.2.
19	14	27.5	8	2	B47393 neuropeptide calla
20	14	27.5	8	2	B45800 serum albumin - do
21	14	27.5	8	4	I54017 graminocyte-colony
22	14	27.5	8	2	S66419 tetrameric protein
23	14	27.5	9	2	S70332 endospem protein,
24	14	27.5	9	2	A29477 diuretic neuropept
25	14	27.5	9	2	S39766 cardiocactive pepti
26	14	27.5	9	2	S77984 cytochrome-c oxida
27	14	27.5	9	2	S66635 alpha-2-macroglobu
28	14	27.5	9	2	S10784 enamelin I - bovin
29	13	25.5	4	2	S53508 starvation-induced

30	13	25.5	6	2	A61049 halo-toxin - Pseud
31	13	25.5	6	2	A44916 mosquitocidal toxi
32	13	25.5	7	2	A15398 choline oxidase (E
33	13	25.5	7	2	I50210 gene c-rel protein
34	13	25.5	7	2	E48394 glycoprotein compo
35	13	25.5	8	2	S08995 hypertrehalosemic
36	13	25.5	8	2	S08996 hypertrehalosemic
37	13	25.5	8	2	A49823 adipoiknetic hormo
38	13	25.5	8	2	B49823 adipoiknetic hormo
39	13	25.5	8	2	A44960 neuropeptide Led-C
40	13	25.5	8	2	B44960 neuropeptide Led-C
41	13	25.5	8	2	A43976 hypertrehalosemic
42	13	25.5	8	2	B43976 hypertrehalosemic
43	13	25.5	8	2	PH1407 Ig heavy chain V r
44	13	25.5	8	2	PL0184 capsid protein Vp-
45	13	25.5	8	2	B39745 endoglycosylcerami

ALIGNMENTS

RESULT 1
 S70345 amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragments)
 C:Species: Aspergillus niger
 C>Date: 19-Mar-1998 #sequence_#revision 17-Apr-1998 #text_change 17-Apr-1998
 C:Accession: S70345
 R:Frederic, I.; Pec, P.; Luhova, L.; Toyama, H.; Matsushita, K.; Hirota, S.; Kitagawa, T.
 Biochim. Biophys. Acta 1295, 59-72, 1996
 A:Title: Two amine oxidases from Aspergillus niger AKU 3302 contain topa quinone as the
 A:Reference number: S70344; MUID:96283794; PMID:8679675
 A:Accession: S70345
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5;6-9<FRS>
 C:Keywords: oxidoreductase

Query Match Similarity 37.3%; Score 19; DB 2; Length 9;
 Best Local 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 PNAPY 8
 |||
 Db 5 PNKEY 9

RESULT 2
 D48186 ATPase R1 subunit - wood tobacco (fragment)
 C:Species: Nicotiana glauca (wood tobacco)
 C>Date: 16-Feb-1994 #sequence_#revision 18-Nov-1994 #text_change 23-Feb-1997
 C:Accession: D48186
 R:De Paape, R.; Forchioni, A.; Chetrit, P.; Vedel, F.
 Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993
 A:Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase
 A:Reference number: A48186; MUID:93317598; PMID:8327463
 A:Accession: D48186
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9<DB1>
 A:Experimental source: Pollen
 A>Note: sequence extracted from NCBI backbone (NCBI:P:134871)

Query Match Similarity 35.3%; Score 18; DB 2; Length 9;
 Best Local 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 APY 8
 |||
 Db 6 APY 8

RESULT 3

PH1408
 Ig heavy chain V region - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C/Accession: PH1408; PH1405
 R/Shirayama, T.; Miyazoe, T.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Teraoka, M.; Exp. Med. 176, 1209-1214, 1992
 A/Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in La virus.
 A/Reference number: PH1403; MUID:93018837; PMID:1402663
 A/Accession: PH1408
 A/Molecule type: DNA
 A/Residues: 177 <SH1>
 A/Experimental source: clone micro m+ 46-12-2
 A/Accession: PH1405
 A/Molecule type: DNA
 A/Residues: 1-7 <SH12>
 A/Experimental source: clone micro m+ 46-6
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 17; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RMPF 4
 | | | |
 | | | |
 Db 4 RRPFP 7

RESULT 4
 JS0302
 xenopsin-related peptide 2 - turkey
 N/Contains: xenopsin-related peptide 1
 C/Species: Meleagris gallopavo (common turkey)
 C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Aug-2000
 C/Accession: JS0302
 R/Carraway, R.E.; Cochran, D.E.; Mitra, S.P.
 Regul. Pept. 22, 303-314, 1988
 A/Title: Xenopsin-related peptide generated in avian gastric extracts.
 A/Reference number: JS0302; MUID:89042995; PMID:2460902
 A/Accession: JS0302
 A/Molecule type: protein
 A/Residues: 1-9 <CAR>
 C/Comment: The peptides are present within several tissues primarily in large molecular C/Superfamily: yeast coatomer complex alpha chain; WD repeat homology
 C/Keywords: neuropeptide
 F:1-9/Product: xenopsin-related peptide 2 #status experimental <XP2>
 F:2-9/Product: xenopsin-related peptide 1 #status experimental <XP1>

Query Match 33.3%; Score 17; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNAPLY 9
 | | | |
 | | | |
 Db 3 PKRPWI 8

RESULT 5
 A60320
 xenopsin-related peptide 2 - rat
 N/Contains: xenopsin-related peptide 1
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 18-Aug-2000
 C/Accession: A60320
 R/Carraway, R.E.; Mitra, S.P.; Muraki, K.
 Regul. Pept. 29, 229-239, 1990
 A/Title: Isolation and structures of xenopsin-related peptides from rat stomach, liver and spleen.
 A/Reference number: A60320; MUID:91018491; PMID:2217904
 A/Accession: A60320
 A/Molecule type: protein
 A/Residues: 1-9 <CAR>

A/Note: the authors purified these peptides from pepsin-treated extracts of stomach, liver
 C/Comment: Xenopsin and xenopsin-related peptides are similar to neurotensin in sequence
 C/Superfamily: yeast coatomer complex alpha chain; WD repeat homology
 C/Keywords: neuropeptide
 F:1-9/Product: xenopsin-related peptide 2 #status experimental <MAT1>
 F:2-9/Product: xenopsin-related peptide 1 #status experimental <MAT2>

Query Match 33.3%; Score 17; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNAPLY 9
 | | | |
 | | | |
 Db 3 PKRPWI 8

RESULT 6
 PL0139
 carbon-monoxide dehydrogenase (BC 1.2.99.2) large chain - Pseudomonas carboxydoflava (fr
 C/Species: Pseudomonas carboxydoflava
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
 C/Accession: PL0139
 R/Krutz, M.; Hugiendieck, I.; Herwig, S.; Meyer, O.
 Arch. Microbiol. 152, 335-341, 1989
 A/Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotropi
 A/Reference number: PL0139; MUID:90055678; PMID:2818128
 A/Accession: PL0139
 A/Molecule type: protein
 A/Residues: 1-9 <KRA>
 A/Note: 2-Met is also found
 C/Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me
 C/Keywords: oxidoreductase

Query Match 33.3%; Score 17; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 NMP 7
 | | | |
 | | | |
 Db 2 NMP 4

RESULT 7
 S21230
 dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
 C/Species: Ptychocheilus bicolor (two-colored leaf frog)
 C/Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
 C/Accession: S21230
 R/Mignogna, G.; Severini, C.; Simeone, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
 FEBS Lett. 302, 151-154, 1992
 A/Title: Identification and characterization of two dermorphins from skin extracts of th
 A/Reference number: S21152; MUID:92339502; PMID:1633846
 A/Accession: S21230
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-7 <MTG>
 C/Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 31.4%; Score 16; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 PPN 5
 | | |
 | | |
 Db 5 YPN 7

RESULT 8
 I57018
 gene C1tr protein - mouse (fragment)
 C/Species: Mus sp. (mouse)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Feb-1997
 C/Accession: I57018

R:Dorin, J.R.; Stevenson, B.J.; Fleming, S.; Alton, E.W.; Dickinson, P.; Porteous, D.J.
 Mamm. Genome 5: 465-472, 1994
 A:Title: Long-term survival of the exon 10 insertional cystic fibrosis mutant mouse is a
 A:Reference number: 157018; MUID:95037043; PMID:7949729
 A:Accession: 157018
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-8 <RRS>
 A:Cross-references: GB:S74246; MUID:9710482
 C:Genetics:
 A:Gene: Cftr

Query Match 31.4%; Score 16; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 4 PNPAL 7
 Db 2 PNDPDM 5

RESULT 9

A44787
 calliFMRamide 10 - bluebottle fly (Calliphora vomitoria)
 C:Species: Calliphora vomitoria
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
 C:Accession: A44787
 R:Duve, H.; Johnson, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
 Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
 A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desl
 A:Reference number: A41978; MUID:92196111; PMID:1549595
 A:Accession: A44787
 A:Status: preliminary
 A:Molecule type: Protein
 A:Residues: 1-9 <DUV>
 C:Keywords: amidated carboxyl end; neuropeptide
 F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 31.4%; Score 16; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 4 PNPAL 9
 Db 2 PNRDPM 7

RESULT 10

D41978
 calliFMRamide 4 - bluebottle fly (Calliphora vomitoria)
 C:Species: Calliphora vomitoria
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
 C:Accession: D41978
 R:Duve, H.; Johnson, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
 Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
 A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desl
 A:Reference number: A41978; MUID:92196111; PMID:1549595
 A:Accession: D41978
 A:Status: preliminary
 A:Molecule type: Protein
 A:Residues: 1-9 <DUV>
 C:Keywords: amidated carboxyl end; neuropeptide
 F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 31.4%; Score 16; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 4 PNPAL 9
 Db 2 PNDPDM 7

RESULT 11
 S15596
 orf3 rara 5'-region - human
 C:Species: Homo sapiens (man)
 C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
 C:Accession: S15596
 R:Brand, N.J.; Peckovich, M.; Chambon, P.
 Nucleic Acids Res. 18, 6799-6806, 1990
 A:Title: Characterization of a functional promoter for the human retinoic acid receptor-
 A:Reference number: S15594; MUID:91088249; PMID:2175878
 A:Accession: S15596
 A:Molecule type: DNA
 A:Residues: 1-6 <BRA>
 A:Cross-references: EMBL:X56058; NID:935876
 A:Note: This ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0
 C:Comment: This sequence is not thought to be translated.
 C:Genetics:
 A:Gene: GDB:RARA
 A:Cross-references: GDB:120337; OMIM:180240
 A:Map position: 17q12-17q12

Query Match 29.4%; Score 15; DB 4; Length 6;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 MPANA 6
 Db 1 MAPSA 5

RESULT 12

S66607
 quinoline 2-oxidoreductase beta chain - Comamonas testosteroni (fragment)
 C:Species: Comamonas testosteroni
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C:Accession: S66607
 R:Schach, S.; Tshisnuka, B.; Fezner, S.; Lalgens, F.
 Eur. J. Biochem. 232, 535-544, 1995
 A:Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from
 A:Reference number: S66606; MUID:96035889; PMID:7556204
 A:Accession: S66607
 A:Molecule type: Protein
 A:Residues: 1-9 <SCH>
 A:Experimental source: strain 63

Query Match 29.4%; Score 15; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 PPNAPY 8
 Db 3 PPARAY 8

RESULT 13

A61620
 locustamyotroptin III - migratory locust
 C:Species: Locusta migratoria (migratory locust)
 C:Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
 C:Accession: A61620
 R:Schroofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
 Insect Biochem. Mol. Biol. 22, 447-452, 1992
 A:Title: Isolation, identification and synthesis of locustamyotroptin III and IV, two add
 A:Reference number: A61620
 A:Accession: A61620
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <SCH>
 C:Keywords: amidated carboxyl end; neuropeptide
 F:9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 29.4%; Score 15; DB 2; Length 9;
 Best Local Similarity 44.4%; Pred. No. 2.8e+05;

Oy 3 PPNAPY 8
 Db 3 PPARAY 8

Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RMPFNAPYL 9

Db 1 RQQPFVPRLL 9

RESULT 14

PH1591
 Ig H chain V-D-J region (wild-type clone 142) - mouse (fragment)
 C:/Species: Mus musculus (house mouse)
 C:/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:/Accession: PH1591
 R:/Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A:/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:/Reference number: PH1580; PMID:93301609; PMID:8315387
 A:/Accession: PH1591
 A:/Molecule type: DNA
 A:/Residues: 19 <LRV>
 A:/Experimental source: bone marrow pre-B lymphocyte
 C:/Keywords: Immunoglobulin

Query Match 29.4%; Score 15; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 APY 8

Db 5 SPY 7

RESULT 15

JS0319
 subesophageal ganglion pentapeptide - house cricket
 C:/Species: Acheta domesticus (house cricket)
 C:/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C:/Accession: JS0319
 R:/Wicker, C.; Wicker, C.
 Comp. Biochem. Physiol. C 88, 185-187, 1987
 A:/Title: Isolation and structure of a peptide isolated from the subesophageal ganglion
 A:/Reference number: JS0319
 A:/Accession: JS0319
 A:/Molecule type: protein
 A:/Residues: 1-5 <WIC>

Query Match 27.5%; Score 14; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 APY 8

Db 3 APY 5

Search completed: January 21, 2004, 08:52:50
 Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 21, 2004, 08:45:45 ; Search time 11 Seconds
(without alignments)
38.476 Million cell updates/sec

Title: US-09-625-963A-1
Perfect score: 51
Sequence: 1 RMFPNAPYL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 251
Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : swissprot_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	22	43.1	UPA7_HUMAN	P30093 homo sapien
2	18	35.3	GRFP_MOUSE	P99025 mus musculu
3	18	35.3	UN06_PIRNS	P81675 pinus pinas
4	18	35.3	B44K_PORGI	P81886 porphyromon
5	17	33.3	PK2_PERRM	P22692 periplaneta
6	17	33.3	OXYF_SCYCA	P42997 scylliorhinu
7	17	33.3	OXYT_OCTVU	P80027 octopus vul
8	16	31.4	FAR4_CALVO	P41859 calliphora
9	16	31.4	FAR4_CALVO	P41865 calliphora
10	16	31.4	FLA2_TREAY	P80159 treponema h
11	16	31.4	UPA3_HUMAN	P30089 homo sapien
12	15	29.4	ALL7_CARMA	P81809 carcinus ma
13	15	29.4	LMT3_LOCM1	P41489 locusta mig
14	14	27.5	SUGA_ACHDO	P19991 acheta dome
15	14	27.5	ALL3_CARMA	P81806 carcinus ma
16	14	27.5	ALL4_CARMA	P81807 carcinus ma
17	14	27.5	ALL5_CARMA	P81808 carcinus ma
18	14	27.5	FARI_HELT	P41871 helisma tr
19	14	27.5	ALL5_CARMA	P81818 carcinus ma
20	14	27.5	ALL6_CARMA	P81819 carcinus ma
21	14	27.5	ALL3_CYDPO	P82154 cydia pomon
22	14	27.5	ALL4_GALVO	P41840 calliphora
23	14	27.5	ALL5_GALVO	P82155 cydia pomon
24	14	27.5	ALL4_CYDPO	P82156 cydia pomon
25	14	27.5	ALL8_CARMA	P81811 carcinus ma
26	14	27.5	ALL9_CARMA	P81812 carcinus ma
27	14	27.5	FUSS_FUSSO	P81010 fusarium so
28	14	27.5	ALL0_CARMA	P81813 carcinus ma
29	14	27.5	COXE_THUOB	P80975 thunnus obe
30	14	27.5	DNF1_LOCM1	P16339 locusta mig
31	14	27.5	NEUX_HUMAN	P04277 homo sapien
32	14	27.5	TKC1_CALVO	P41517 calliphora
33	13	25.5	PAP2_PARMA	P81864 pardachirus

ID	UPA7_HUMAN	STANDARD	PRT	9 AA.
34	P30093			CHOX ALCSP
35	P30093			FAR4_PANRE
36	P30093			NMPL_LERDE
37	P30093			UF04_MOUSE
38	P30093			FAR1_PANRE
39	P30093			FAR4_MACRS
40	P30093			HTF1_PERRM
41	P30093			HTF2_PERRM
42	P30093			HTF_TENNO
43	P30093			PK3_PERRM
44	P30093			UF06_MOUSE
45	P30093			UPA1_HUMAN

ALIGNMENTS

RESULT 1	UPA7_HUMAN	STANDARD	PRT	9 AA.
AC	P30093			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Unknown protein from 2D-page of plasma (Spot 18) (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Plasma;			
RX	MEDLINE=93092937; Pubmed=1459097;			
RA	Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,			
RA	Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,			
RA	Hochstrasser D.F.;			
RT	"Plasma protein map: an update by microsequencing.";			
RL	Electrophoresis 13:707-714 (1992).			
CC	-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN			
CC	PROTEIN IS: 5.05; ITS MW IS: 37 KDa.			
DR	SWISS-2DPAGE; P30093; HUMAN.			
FT	NON_TER	1		
FT	UNSURE	5	5	
FT	NON_TER	9	9	
SO	SEQUENCE	9 AA;	1042 MW;	SC14477AEB0772C7 CRC64;

Query Match	43.1%	Score 22;	DB 1;	Length 9;
Best Local Similarity	42.9%	Pred. No. 1.3e+05;		
Matches	3;	Conservative 1;	Mismatches 3;	Indels 0;
			Gaps	0;

RESULT 2	GRFP_MOUSE	STANDARD	PRT	7 AA.
AC	P99025			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	GFP cyclonhydrolase I feedback regulatory protein (P35) (Fragment).			
DN	GCFR OR GRFP.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Liver;			
RA	Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,			
RA	Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.;			

RA Cowthorne M.;
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.
 CC -1- FUNCTION: MEDIATES TETRAHYDROBIOTERIN INHIBITION OF GTP
 CYCLOHYDROLASE I. THIS INHIBITOR IS REVERSED BY L-PHENYLALANINE
 (BY SIMILARITY).
 CC -1- SUBUNIT: Homodimer (By similarity).
 DR SWISS-2DPAGE; P99025; MOUSE.
 FT INT MET 0
 FT NON_TER 0
 SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

Query Match 35.3%; Score 18; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PYL 9
 Db 1 PYL 3

RESULT 3
 UN06_PINPS STANDARD; PRT; 7 AA.
 AC P81675;
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DR 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of needles (N141) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Coniferales; Pinaceae; Pinus.
 OX NCB1_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins."
 RL Electrophoresis 20:1098-1108(1999).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.6, ITS MW IS: 25 KDa.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 35.3%; Score 18; DB 1; Length 7;
 Best Local Similarity 28.6%; Pred. No. 1.3e+05;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 PPNAPY 8
 Db 1 LYGNLP 7

RESULT 4
 B44K_PORGI STANDARD; PRT; 8 AA.
 AC P81886;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DR 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 44 kDa immunogenic protein (Fragment).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 CC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCB1_TaxID=837;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=VBP 3492;
 RX MEDLINE=20198497; PubMed=10731616;
 RA Norris J.M., Love D.N.;

RT "Serum antibody responses of cats to soluble whole cell antigens of
 RT feline Porphyromonas gingivalis."
 RL Vet. Microbiol. 73:37-49(2000).
 CC -1- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
 KW Antigen.
 FT NON_TER 8
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match 35.3%; Score 18; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 APY 8
 Db 1 APY 3

RESULT 5
 PPK2_PERAM STANDARD; PRT; 8 AA.
 AC P82652;
 DT 16-OCT-2001 (Rel. 40, Created)
 DR 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Pyroklinin-2 (Pea-PK-2) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 OC Insecta; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
 OC Blattidae; Periplaneta.
 OX NCB1_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=97353923; PubMed=9210163;
 RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of two pyrokinins from the
 RT retrocerebral complex of the American cockroach."
 RL Peptides 18:473-478(1997).
 RN [2]
 RP TISSUE SPECIFICITY.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach."
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -1- MASS SPECTROMETRY: MM=883; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro: IPR001484; Pyrokinin.
 DR PROSITE: PS00539; PYROKININ; FALSE_NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 884 MW; C834176DD9D77775 CRC64;

Query Match 33.3%; Score 17; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNPAYL 9
 Db 3 PFAFRL 8

RESULT 6
 OXYF_SCYCA STANDARD; PRT; 9 AA.
 AC P42957;
 DT 01-NOV-1995 (Rel. 32, Created)
 DR 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Phasvatocin.

OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Garcharniformes;
 OC Scyllorhinidae; Scyllorhinus.
 OX NCB1_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pituitary; PubMed=7972045;
 RX MEDLINE=95062247; Chauveau C., Chauvet M.-T., Acher R.;
 RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
 RT "Species evolution of neurohypophysial hormones in cartilaginous
 fishes: asatocin and phasatocin, two oxytocin-like peptides
 isolated from the spotted dogfish (Scyllorhinus caniculus).";
 RT Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
 RL -1- SIMILARITY: DISPLAYS OXYTOCIN ACTIVITY ON RAT UTERUS.
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro; IPR000981; Neurohyp_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.
 FT SEQUENCE 9 AA; 1016 MW; 17EDD76EB4449DB CRC64;
 SQ

Query Match 33.3%; Score 17; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 PNPAP 7
 Db 3 FRNCP 7

RESULT 7
 OXYT OCTVU STANDARD; PRT; 9 AA.
 ID OXYT OCTVU
 AC P80027;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Cephalotocin.
 OS Octopus vulgaris (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Inccirrata; Octopodidae; Octopus.
 OX NCB1_TaxID=6645;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Nerve endings;
 RX MEDLINE=92270139; PubMed=1589145;
 RA Reich G.;
 RT "A new peptide of the oxytocin/vasopressin family isolated from
 nerves of the cephalopod Octopus vulgaris.";
 RT Neurosci. Lett. 134:191-194(1992).
 RL -1- FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA
 CAVA.
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro; IPR000981; Neurohyp_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.
 FT SEQUENCE 9 AA; 1072 MW; 17FF476BB45409DB CRC64;
 SQ

Query Match 33.3%; Score 17; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 PNPAP 7
 Db 3 FRNCP 7

RESULT 8
 FARA CALVO STANDARD; PRT; 9 AA.
 ID FARA CALVO
 AC P41855;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Callipmrfamide 4.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCB1_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Dye H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -phe-Met-Arg-phe-NH2
 neuropeptides (designated callipmrfamides) from the blowfly
 Calliphora vomitoria.";
 RT Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 RL -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 DR PIR; A44787; A44787.
 DR Neuropeptide; Amidation.
 KW MOD_RES 9 9
 FT UNSURE 1 1
 FT SEQUENCE 9 AA; 1183 MW; 31730699CAB6D457 CRC64;
 SQ

Query Match 31.4%; Score 16; DB 1; Length 9;
 Best Local Similarity 33.3%; Pred. No. 1.3e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNPAP 9
 Db 2 PNODFM 7

RESULT 9
 FARA CALVO STANDARD; PRT; 9 AA.
 ID FARA CALVO
 AC P41855;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Callipmrfamide 10.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCB1_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Dye H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -phe-Met-Arg-phe-NH2
 neuropeptides (designated callipmrfamides) from the blowfly
 Calliphora vomitoria.";
 RT Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 RL -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 DR PIR; A44787; A44787.
 DR Neuropeptide; Amidation.
 KW MOD_RES 9 9
 FT UNSURE 1 1
 FT SEQUENCE 9 AA; 1183 MW; 29D00699CAB40457 CRC64;
 SQ

Query Match 31.4%; Score 16; DB 1; Length 9;
 Best Local Similarity 33.3%; Pred. No. 1.3e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNPAPL 9
DB 2 PNRDFM 7

RESULT 10

FLA2_TREHY STANDARD; PRT; 9 AA.
AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein) (Fragment).
GN FLA2.
OS Treponema hydrophilum (Serpulina hydrosymbiotes).
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspirina.
OX NCBI_TaxID=159;
RN [1]
RP SEQUENCE.
RX STRAIN=C5;
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H., Baats F., Van Vorstenbosch C.J.A.H.V.,
RA van der Zelfst B.A.M., Kusters J.G.;
RT "The periplasmic flagella of Serpulina (Treponema) hydrosymbiotes are composed of two sheath proteins and three core proteins."
RL J. Gen. Microbiol. 138:2697-2706 (1992).
CC -1- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.
CC -1- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO SHEATH PROTEINS, FLA1 (44 kDa) AND FLA2 (35 kDa) AROUND A CORE THAT CONTAINS THREE PROTEINS FLA1 (37 kDa), FLA2 (34 kDa) AND FLA3 (32 kDa).
CC -1- SUBCELLULAR LOCATION: Periplasmic flagellum.
KW Flagella; Periplasmic.
FT UNSURE 2
FT UNSURE 8
FT NON TER 9
SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;

Query Match 31.4%; Score 16; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 11
UPA3_HUMAN STANDARD; PRT; 9 AA.
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochrater D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714 (1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
DR SWISS-2DPAGE; P30089; HUMAN.

FT NON TER 1 1
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;
Query Match 31.4%; Score 16; DB 1; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.3e+05;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 12

ALL7_CARMA STANDARD; PRT; 8 AA.
ID ALL7_CARMA
AC P81809; P81804; P81810;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Carcinostatrin 7 [Contains: Carcinostatrin 6; Carcinostatrin 1].
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RX TISSUE=Cerebral ganglion, and thoracic ganglion;
RX MEDLINE=96121193; PubMed=9461295;
RA Duye H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734 (1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Allatostatin; Multigene family.
FT PEPTIDE 1 8 CARCINUSTATIN 7.
FT PEPTIDE 2 8 CARCINUSTATIN 6.
FT PEPTIDE 4 8 CARCINUSTATIN 1.
FT MOD RES 8 AMIDATION.
SQ SEQUENCE 8 AA; 825 MW; 922879CDDB4775BD CRC64;

Query Match 29.4%; Score 15; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
LMT3_LOCOMI STANDARD; PRT; 9 AA.
ID LMT3_LOCOMI
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotroopin 3 (Lom-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygora;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotroopin III and IV, two additional neuropeptides of Locusta migratoria: members of the

RT Locustamyoctropin peptide family.";
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).
 CC -1- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
 (MYOTROPIC ACTIVITY).
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro: IPR001484; Pyrokinin.
 DR PROSITE: PS00539; PYROKININ: 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 1140 MW; DSAELI72C9D776C6 CRC64;

Query Match 29.4%; Score 15; DB 1; Length 9;
 Best Local Similarity 44.4%; Pred. No. 1.3e+05;
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 RMPFNPVYL 9
 DB 1 RQQPFVPRLL 9

RESULT 14
 SUGA_ACHDO STANDARD; PRT; 5 AA.
 ID SUGA_ACHDO STANDARD; PRT; 5 AA.
 AC P19951;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Suboesophageal ganglion pentapeptide.
 OS Acheta domesticus (House cricket).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
 CC Acheta.
 OX NCBI_TaxID=6997;
 RN [1]
 RP SEQUENCE.
 RA Wicker C., Wicker C.;
 RT "Isolation and structure of a peptide isolated from the
 suboesophageal ganglion of Acheta domesticus (orthoptera).";
 RL Comp. Biochem. Physiol. 88C:185-187(1987).
 CC -1- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
 CC GANGLIA.
 DR PIR: JS0319; JS0319.
 SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 APY 8
 DB 3 APV 5

RESULT 15
 ALI3_CARMA STANDARD; PRT; 7 AA.
 ID ALI3_CARMA STANDARD; PRT; 7 AA.
 AC P81806;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 3.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RT TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINS=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;

RT "Isolation and identification of multiple neuropeptides of the
 RL allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATTIN FAMILY.
 KW Neuropeptide; Multigene family.
 SQ SEQUENCE 7 AA; 796 MW; 672879CDBC8476B70 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PY 8
 DB 2 PY 3

Search completed: January 21, 2004, 08:51:29
 Job time : 13 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 21, 2004, 08:48:55 ; Search time 34 Seconds
(without alignments)
68.308 Million cell updates/sec

Title: US-09-625-963A-1
Perfect score: 51
Sequence: 1 RMPFNAPYL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 775

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mbc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	39.2	9	4 Q9UMF3	Q9UMF3 homo sapien
2	17	33.3	9	4 Q9U50	Q9U50 homo sapien
3	17	33.3	9	4 Q96T78	Q96T78 homo sapien
4	17	33.3	9	10 P82429	P82429 nicotiana t
5	16	31.4	8	2 Q9RT72	Q9RT72 escherichia
6	16	31.4	9	3 Q9P8B5	Q9P8B5 Kluyveromyc
7	15	29.4	8	5 Q9TWH6	Q9TWH6 peritremis
8	15	29.4	8	10 Q8GTG5	Q8GTG5 Lycopersico
9	15	29.4	9	4 Q9UCG8	Q9UCG8 homo sapien
10	15	29.4	9	4 Q9H522	Q9H522 homo sapien
11	15	29.4	9	10 Q9S8U8	Q9S8U8 oryza sativ
12	15	27.5	7	8 Q98866	Q98866 spinnacia ol
13	14	27.5	7	15 Q07624	Q07624 rous sarcom
14	14	27.5	8	3 P82858	P82858 puccinia re
15	14	27.5	8	8 Q8W8G2	Q8W8G2 diadema sav
16	14	27.5	8	8 Q8W8G4	Q8W8G4 diadema mex

RESULT 1	ID	Q9UMF3	PRELIMINARY;	PRT;	9 AA.	ALIGNMENTS
17	14	27.5	8	8 Q8W8G5	Q8W8G5 diadema ant	
18	14	27.5	8	8 Q8W8G3	Q8W8G3 diadema pau	
19	14	27.5	8	8 Q8W8R5	Q8W8R5 diadema pau	
20	14	27.5	8	11 Q8K3Z7	Q8K3Z7 mus musculus	
21	14	27.5	8	11 Q9P940	Q9P940 mus musculus	
22	14	27.5	9	2 P83157	P83157 anabaena sp	
23	14	27.5	9	6 Q9TRU7	Q9TRU7 bos taurus	
24	14	27.5	9	8 Q8WFS4	Q8WFS4 diadema mex	
25	14	27.5	9	8 Q8W8X4	Q8W8X4 diadema mex	
26	14	27.5	9	8 Q9T2K9	Q9T2K9 spinnacia ol	
27	14	27.5	9	8 Q8W8W5	Q8W8W5 diadema set	
28	14	27.5	9	8 Q8W8W6	Q8W8W6 diadema ant	
29	14	27.5	9	12 Q67605	Q67605 squash leaf	
30	14	27.5	9	12 Q67606	Q67606 squash leaf	
31	13	25.5	8	2 Q9AGP4	Q9AGP4 arthrobacte	
32	13	25.5	8	2 Q49534	Q49534 mycoplasma	
33	13	25.5	9	2 Q99193	Q99193 pseudomonas	
34	13	25.5	9	4 Q9UKJ6	Q9UKJ6 homo sapien	
35	13	25.5	9	4 Q9UC36	Q9UC36 homo sapien	
36	13	25.5	9	6 Q28121	Q28121 bos taurus	
37	13	25.5	9	12 Q71066	Q71066 canine dist	
38	13	25.5	9	16 Q935G1	Q935G1 salmonella	
39	12	23.5	8	4 Q9P0K3	Q9P0K3 homo sapien	
40	12	23.5	8	10 P82324	P82324 pisum sativ	
41	12	23.5	8	11 Q9JID7	Q9JID7 mesocricetu	
42	12	23.5	8	11 P82598	P82598 rattus norv	
43	12	23.5	8	12 Q9W7J3	Q9W7J3 pseudorabie	
44	12	23.5	8	12 Q90345	Q90345 hepaticis g	
45	12	23.5	8	13 Q8JFN8	Q8JFN8 gallus gall	

RESULT 2	ID	Q9U50	PRELIMINARY;	PRT;	8 AA.
1	9	1067	MW;	DD46A76DCC6C76046	CRC64;
2	9	1067	MW;	DD46A76DCC6C76046	CRC64;
3	9	1067	MW;	DD46A76DCC6C76046	CRC64;
4	9	1067	MW;	DD46A76DCC6C76046	CRC64;
5	9	1067	MW;	DD46A76DCC6C76046	CRC64;
6	9	1067	MW;	DD46A76DCC6C76046	CRC64;
7	9	1067	MW;	DD46A76DCC6C76046	CRC64;
8	9	1067	MW;	DD46A76DCC6C76046	CRC64;
9	9	1067	MW;	DD46A76DCC6C76046	CRC64;
10	9	1067	MW;	DD46A76DCC6C76046	CRC64;
11	9	1067	MW;	DD46A76DCC6C76046	CRC64;
12	9	1067	MW;	DD46A76DCC6C76046	CRC64;
13	9	1067	MW;	DD46A76DCC6C76046	CRC64;
14	9	1067	MW;	DD46A76DCC6C76046	CRC64;
15	9	1067	MW;	DD46A76DCC6C76046	CRC64;
16	9	1067	MW;	DD46A76DCC6C76046	CRC64;
17	9	1067	MW;	DD46A76DCC6C76046	CRC64;
18	9	1067	MW;	DD46A76DCC6C76046	CRC64;
19	9	1067	MW;	DD46A76DCC6C76046	CRC64;
20	9	1067	MW;	DD46A76DCC6C76046	CRC64;
21	9	1067	MW;	DD46A76DCC6C76046	CRC64;
22	9	1067	MW;	DD46A76DCC6C76046	CRC64;
23	9	1067	MW;	DD46A76DCC6C76046	CRC64;
24	9	1067	MW;	DD46A76DCC6C76046	CRC64;
25	9	1067	MW;	DD46A76DCC6C76046	CRC64;
26	9	1067	MW;	DD46A76DCC6C76046	CRC64;
27	9	1067	MW;	DD46A76DCC6C76046	CRC64;
28	9	1067	MW;	DD46A76DCC6C76046	CRC64;
29	9	1067	MW;	DD46A76DCC6C76046	CRC64;
30	9	1067	MW;	DD46A76DCC6C76046	CRC64;
31	9	1067	MW;	DD46A76DCC6C76046	CRC64;
32	9	1067	MW;	DD46A76DCC6C76046	CRC64;
33	9	1067	MW;	DD46A76DCC6C76046	CRC64;
34	9	1067	MW;	DD46A76DCC6C76046	CRC64;
35	9	1067	MW;	DD46A76DCC6C76046	CRC64;
36	9	1067	MW;	DD46A76DCC6C76046	CRC64;
37	9	1067	MW;	DD46A76DCC6C76046	CRC64;
38	9	1067	MW;	DD46A76DCC6C76046	CRC64;
39	9	1067	MW;	DD46A76DCC6C76046	CRC64;
40	9	1067	MW;	DD46A76DCC6C76046	CRC64;
41	9	1067	MW;	DD46A76DCC6C76046	CRC64;
42	9	1067	MW;	DD46A76DCC6C76046	CRC64;
43	9	1067	MW;	DD46A76DCC6C76046	CRC64;
44	9	1067	MW;	DD46A76DCC6C76046	CRC64;
45	9	1067	MW;	DD46A76DCC6C76046	CRC64;

DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Lactophilin-2 (Fragment).
 GN LPHH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99153747; PubMed=10030676;
 RA White G.R.M., Varley J.M., Heighway J.;
 RT "Isolation and characterisation of a human homologue of the
 RT Lactophilin gene from a region of 1p31.1 implicated in breast
 RT cancer.";
 RL Oncogene 17:3513-3519 (1998).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20225451; PubMed=10760572;
 RA White G.R.M., Varley J.M., Heighway J.;
 RT "Genomic structure and expression profile of LPHH1, a 7TM gene
 RT variably expressed in breast cancer cell lines.";
 RL Biochim. Biophys. Acta 1491:75-92(2000).
 DR EMBL; AJ244509; CAB60204.1; -.
 FT NON_TER 1 1
 FT NON_TER 8 8
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 1025 MW; 4D59D763344AAB08 CRC64;

Query Match 33.3%; Score 17; DB 4; Length 8;
 Best Local Similarity 40.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 NAYPL 9
 DB 4 NKPF 8

RESULT 3
 Q96T78 PRELIMINARY; PRT; 9 AA.
 AC Q96T78;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Contactin-associated protein 2 (Fragment).
 GN CNTNAP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21250995; PubMed=11352571;
 RA Nakabayashi K., Scherer S.W.;
 RT "The human contactin-associated protein 2 (CNTNAP2) spans over 2 Mb of
 RT DNA at chromosome 7q35."
 RL Genomics 73:108-112(2001).
 DR EMBL; AF318295; AAK49906.1; -.
 FT NON_TER 1 1
 FT NON_TER 9 9
 FT NON_TER 1 1
 SQ SEQUENCE 9 AA; 1080 MW; 9139A2D5A77B51EA CRC64;

Query Match 33.3%; Score 17; DB 4; Length 9;
 Best Local Similarity 33.3%; Pred. No. 8.3e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 FPNAPY 8
 DB 4 YPSVSY 9

P82429 PRELIMINARY; PRT; 9 AA.
 ID P82429
 AC P82429
 DT 01-JUN-2000 (TREMBlrel. 14, Created)
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE 44 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asceridae; Lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE. PRTT HAVANA;
 RC STRAIN=cv. Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojlasek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture.";
 RL Planta 0.0-0(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL.
 CC -1- TISSUE SPECIFICITY: XYLEM.
 FT NON_TER 9 9
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 986 MW; C22CCAAD6C77776 CRC64;

Query Match 33.3%; Score 17; DB 10; Length 9;
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PNAYPL 9
 DB 4 PNDPFL 9

RESULT 5
 Q9R7T2 PRELIMINARY; PRT; 8 AA.
 AC Q9R7T2
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Hypothetical 1.0 kDa protein (Fragment).
 GN YFG.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sangei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
 RT to the 12.7-28.0 min Region on the Linkage Map.";
 RL DNA Res. 3:137-155(1996).
 DR EMBL; D90705; BAA35310.1; -.
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;

Query Match 31.4%; Score 16; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 PYL 9
 DB 2 PYI 4

RESULT 6
 Q9P8E5 PRELIMINARY; PRT; 9 AA.
 AC Q9P8E5; :
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE HIS4 protein (Fragment).
 GN HIS4.
 OS *Kluyveromyces fragilis* (yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL-Y1140;
 RX MEDLINE=99448382; PubMed=10518937;
 RA Imanis-Maciras M., Esperanza Cerdan B., Fraire-Picos M.A.;
 RT "Kluyveromyces fragilis HIS4 transcriptional regulation: similarities
 RL and differences to Saccharomyces cerevisiae HIS4 gene."
 RL FEBS Lett. 458:72-76(1999).
 DR EMBL; AJ238494; CAB87125.1; -.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

Query Match 31.4%; Score 16; DB 3; Length 9;
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 MFNPAP 7
 Db 1 MLPVVP 6

RESULT 7
 Q9TWH6 PRELIMINARY; PRT; 8 AA.
 AC Q9TWH6; :
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE BIOACTIVE peptide P4-PUTATIVE ESOPHAGEAL NEUROREGULATOR.
 OS *Perinereis vancaurica*.
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Acticulata;
 CC Phyllodoctida; Nereididae; Perinereis.
 OX NCBI_TaxID=6355;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=95323338; PubMed=7599979;
 RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.,
 RA Fujita T., Minakata H., Nomoto K.;
 RT "Isolation and characterization of four novel bioactive peptides from
 RT a polychaete annelid, *Perinereis vancaurica*."
 RL Comp. Biochem. Physiol. C, Pharmacol. Toxicol. Endocrinol. 110:297-
 RL 304(1995).
 SQ SEQUENCE 8 AA; 989 MW; 954772CA87B0B59 CRC64;

Query Match 29.4%; Score 15; DB 5; Length 8;
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 NAPP 8
 Db 5 DVPP 8

RESULT 8
 Q8GTG5 PRELIMINARY; PRT; 8 AA.
 AC Q8GTG5; :
 DT 01-MAR-2003 (TReMBLrel. 23, Created)

DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE WRKY transcription factor lrd-1 splice variant 2 (Fragment).
 OS *Lycopersicon esculentum* (Tomato).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Money Maker; TISSUE=Leaf;
 RA Cagna G., Boes A., Ulker B., Zhou A., Wanke D., Somssich I.E.;
 RT "Comparison of WRKY group II transcription factors from plants."
 RL Submitted (SFP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY157059; AAN71729.1; -.
 FT NON_TER
 SQ SEQUENCE 8 AA; 917 MW; 59177B4775B87330 CRC64;

Query Match 29.4%; Score 15; DB 10; Length 8;
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 APY 8
 Db 4 SPY 6

RESULT 9
 Q9UCS8 PRELIMINARY; PRT; 9 AA.
 AC Q9UCS8; :
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Apolipoprotein A-I (Fragment).
 OS *Homo sapiens* (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=92075698; PubMed=1742316;
 RA Ehhholm C., Bozas S.E., Tenkanen H., Kirzbaum J., Meteo J.,
 RA Murphy B., Walker I.D.;
 RT "The apolipoprotein A-I binding protein of placenta and the Sp-40,40
 RT protein of human blood are different proteins which both bind to
 RT apolipoprotein A-I."
 RL Biochim. Biophys. Acta 1086:255-260(1991).
 FT NON_TER
 SQ SEQUENCE 9 AA; 981 MW; 7BE37775A6C7776B CRC64;

Query Match 29.4%; Score 15; DB 4; Length 9;
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PNP 7
 Db 4 POSP 7

RESULT 10
 Q9H522 PRELIMINARY; PRT; 9 AA.
 AC Q9H522; :
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE BA90M5.3 (HCG-1) (Fragment).
 GN BA90M5.3.
 OS *Homo sapiens* (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCB1_TaxID=96606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tromans A.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL139188; CAC15103.1; -
 FT NON TER 9
 SO SEQUENCE 9 AA; 951 MW; 96A3ADC72C455A5 CRC64;

Query Match 29.4%; Score 15; DB 4; Length 9;
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 MFPNP 7
 DB 1 MSSNP 6

RESULT 11

ID Q9S8J8 PRELIMINARY; PRT; 9 AA.
 AC Q9S8J8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE ORYZATENSIN-BIOACTIVE peptide.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrharioideae; Oryzaceae; Oryza.
 OX NCB1_TaxID=4530;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95102521; PubMed=78041411;
 RA Takahashi M., Moriyuchi S., Yoshikawa M., Sasaki R.;
 RT "Isolation and characterization of oryzatensin: a novel bioactive
 RT peptide with ileum-contracting and immunomodulating activities derived
 RT from rice albumin.";
 RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
 DR Gramene; Q9S8J8; -
 SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 29.4%; Score 15; DB 10; Length 9;
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MFP 4
 DB 4 MYP 6

RESULT 12

ID Q98866 PRELIMINARY; PRT; 7 AA.
 AC Q98866;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE Cytochrome b/F subunit IV (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCB1_TaxID=3562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86120353; PubMed=3003688;
 RA Siben-Muelier G., Halliack R.B., Alt J., Westhoff P., Herrmann R.G.;
 RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal
 RT Nucleic Acids Res. 14:1029-1044(1986).
 DR EMBL; X03496; CAA27215.1; -

Query Match 27.5%; Score 14; DB 8; Length 7;
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 PYL 9
 DB 4 PFL 6

RESULT 13

ID Q07624 PRELIMINARY; PRT; 7 AA.
 AC Q07624;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE UORF1.
 OS Rous sarcoma virus (strain Prague C).
 OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
 OX NCB1_TaxID=11888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93010967; PubMed=1327749;
 RA Donze O., Spahr P.F.;
 RT "Role of the open reading frames of Rous sarcoma virus leader RNA in
 RT translation and genome packaging.";
 RL EMBO J. 11:3747-3757(1992).
 DR EMBL; X67587; CAA47862.1; -
 SQ SEQUENCE 7 AA; 672 MW; 776045A7687DD6F0 CRC64;

Query Match 27.5%; Score 14; DB 15; Length 7;
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PNP 7
 DB 4 PSP 7

RESULT 14

ID P82858 PRELIMINARY; PRT; 8 AA.
 AC P82858;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Uricase (EC 1.7.3.3) (urate oxidase) (Fragment).
 OS Puccinia recondita f. sp. triseti.
 OC Eukaryota; Fungi; Basidiomycota; Urediniomycetes; Urediniomycetidae;
 OC Uredinales; Pucciniales; Puccinia.
 OX NCB1_TaxID=142679;
 RN [1]
 RP SEQUENCE, FUNCTION, AND DEVELOPMENTAL STAGE.
 RC TISSUE=SPORE;
 RA Aguilar M., Montalbini P., Pineda M.;
 RT Submitted (NOV-2000) to the SWISS-PROT data bank.
 CC -1- FUNCTION: INVOLVED IN HOST-PARASITE RELATIONSHIP BETWEEN PLANTS
 CC AND FUNGI.
 CC -1- CATALYTIC ACTIVITY: URATE + O(2) + H(2)O = 5-HYDROXYISOURATE +
 CC H(2)O(2) (5-HYDROXYISOURATE DECOMPOSE TO FORM ALANTOIN).
 CC -1- SUBCELLULAR LOCATION: PEROXISOMAL (BY SIMILARITY).
 CC -1- DEVELOPMENTAL STAGE: GERMINATION.
 CC -1- SIMILARITY: BELONGS TO THE URICASE FAMILY.
 DR Interpro: IPR002042; Uricase.
 DR PROSITE; PS00366; URICASE; PARTIAL.
 DR Oxidoreductase; Purine metabolism; Peroxisome.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 777 MW; 98C1ADD735B9D76D CRC64;

Query Match 27.5%; Score 14; DB 15; Length 7;
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 27.5%; Score 14; DB 3; Length 8;
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 APYL 8
 | | | | | | | |
 Db 1 APF 3

RESULT 15

Q8W8G2 PRELIMINARY; PRT; 8 AA.
 AC Q8W8G2:
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Cytochrome oxidase subunit II (Fragment).
 GN COII.
 OS Diadema savigny (longspine black urchin).
 OC Microchordion.
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinozoa; Euechinozoa; Diadematacea; Diadematozoa; Diadematozoa;
 OC Diadema.
 OX NCBI_TaxID=105360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DP751, SA2, SA7, SA10, GSA1, GSA3, GSA4, DOK17, and DOK105;
 RX MEDLINE=21323357; PubMed=11430656;
 RA Leesios H.A., Keasing B.D., Pearce J.S.;
 RT "Population structure and speciation in tropical seas: global
 RT phylogeography of the sea urchin Diadema."
 RL Evolution 55:955-975 (2001).
 DR EMBL; AY013065; AAL33860.1; -
 DR EMBL; AY013080; AAL33861.1; -
 DR EMBL; AY013083; AAL33862.1; -
 DR EMBL; AY013086; AAL33863.1; -
 DR EMBL; AY013088; AAL33864.1; -
 DR EMBL; AY013090; AAL33865.1; -
 DR EMBL; AY013091; AAL33867.1; -
 DR EMBL; AY013102; AAL33868.1; -
 DR EMBL; AY013103; AAL33869.1; -
 KW Mitochondrion.
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 1037 MW; 701B173B46DDC2D3 CRC64;
 Query Match 27.5%; Score 14; DB 8; Length 8;
 Best Local Similarity 75.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 APYL 9
 | | | | | | | |
 Db 3 AOYL 6

Search completed: January 21, 2004, 08:52:17
 Job time : 36 secs

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PS Claim 1; Page 74; 93pp; English.
 CC The present sequence is peptide epitope WT126-34, produced by WT1
 CC expressing cells and found at residues 126-134 of the WT1 protein, which
 CC is recognized by cytotoxic T lymphocytes. WT1 is aberrantly expressed in
 CC leukemia, breast cancer, melanoma and ovarian cancer. The peptide can
 CC be used as a vaccine to stimulate the elimination, by cytotoxic T
 CC lymphocytes, of cancer cells aberrantly expressing WT1. In addition, the
 CC nucleic acid encoding the peptide may also be used in the same manner.
 CC Alternatively, the peptide may be used in vitro to produce activated
 CC cytotoxic T lymphocytes.

XX Sequence 9 AA;
 SQ Query Match 100.0%; Score 51; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9
 DB 1 RMFPNAPYL 9

RESULT 2
 AA98670 AAY98670 standard; Peptide; 9 AA.

AC AAY98670;
 DT 31-JUL-2000 (first entry)

DE WT1 derived immunogenic peptide SEQ ID NO:185.

XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
 XX metastatic disease; mouse; human; Wilm's tumour; immune response;
 XX vaccine.

OS Homo sapiens.

PN WO200018795-A2.

XX 06-APR-2000.

PF 30-SEP-1999; 99WO-US22819.

PR 30-SEP-1998; 98US-0164223.

PR 25-MAR-1999; 99US-0276484.

PA (CORI-) CORIXA CORP.

PI (GAIG/) GAIGER A.

DR Gaiger A, Cheever M;

XX WPI; 2000-293107/25.

PT Novel polypeptides comprising an immunogenic portion of a native WT1
 PT polypeptide, useful for inhibiting the development of malignant
 PT diseases associated with WT1 expression e.g. leukemia or cancer

XX Claim 4; Page 171; 193pp; English.

XX The present invention describes polypeptides (I) comprising an
 CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,
 CC WT1, (or variants of the immunogenic portion retaining the ability to
 CC react with WT1-specific antisera and/or T-cell lines or clones) and
 CC comprising 16 consecutive amino acids (aa) or less of a native WT1
 CC polypeptide. The polypeptides are useful therapeutically and to
 CC manufacture medicaments for enhancing/inducing an immune response in
 CC patients. The polypeptides, mimetics or polynucleotides can be included
 CC with a carrier/excipient in pharmaceutical compositions or with a
 CC non-specific immune response enhancer (e.g. an adjuvant or enhancer
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
 CC compositions and vaccines can be administered to human patients to

CC enhance or induce an immune response specific for WT1 or a cell
 CC expressing WT1, useful to inhibit the development of malignant diseases
 CC associated with WT1 expression, e.g. leukemia (especially acute/chronic
 CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).
 CC AAY98501 to AAY98811 represent polypeptide sequences, and AAY13848 to
 CC AAY13862 represent PCR primers, used in the exemplification of the
 CC present invention.

XX Sequence 9 AA;
 SQ Query Match 100.0%; Score 51; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9
 DB 1 RMFPNAPYL 9

RESULT 3
 AA98778 AAY98778 standard; Peptide; 9 AA.

AC AAY98778;
 DT 31-JUL-2000 (first entry)

DE WT1 derived immunogenic peptide SEQ ID NO:293.

XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
 XX metastatic disease; mouse; human; Wilm's tumour; immune response;
 XX vaccine.

OS Mus musculus.

PN WO200018795-A2.

XX 06-APR-2000.

PF 30-SEP-1999; 99WO-US22819.

PR 30-SEP-1998; 98US-0164223.

PR 25-MAR-1999; 99US-0276484.

PA (CORI-) CORIXA CORP.

PI (GAIG/) GAIGER A.

DR Gaiger A, Cheever M;

XX WPI; 2000-293107/25.

PT Novel polypeptides comprising an immunogenic portion of a native WT1
 PT polypeptide, useful for inhibiting the development of malignant
 PT diseases associated with WT1 expression e.g. leukemia or cancer

XX Claim 4; Page 186; 193pp; English.

XX The present invention describes polypeptides (I) comprising an
 CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,
 CC WT1, (or variants of the immunogenic portion retaining the ability to
 CC react with WT1-specific antisera and/or T-cell lines or clones) and
 CC comprising 16 consecutive amino acids (aa) or less of a native WT1
 CC polypeptide. The polypeptides are useful therapeutically and to
 CC manufacture medicaments for enhancing/inducing an immune response in
 CC patients. The polypeptides, mimetics or polynucleotides can be included
 CC with a carrier/excipient in pharmaceutical compositions or with a
 CC non-specific immune response enhancer (e.g. an adjuvant or enhancer
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
 CC compositions and vaccines can be administered to human patients to
 CC enhance or induce an immune response specific for WT1 or a cell
 CC expressing WT1, useful to inhibit the development of malignant diseases
 CC associated with WT1 expression, e.g. leukemia (especially acute/chronic

KW Mouse; Wilms' tumour; WT1; pleural mesothelioma; antigen; leukemia; acute myeloid leukemia; ALL; myelodysplastic syndromes; myeloproliferative syndrome; cancer; cytostatic.
 KW acute lymphocytic leukemia; ALL; myelodysplastic syndromes;
 KW myeloproliferative syndrome; cancer; cytostatic.
 OS Mus musculus.
 XX WO200162920-A2.
 XX PD 30-AUG-2001.
 XX PF 22-FEB-2001; 2001WO-US05702.
 XX PR 22-FEB-2000; 2000US-184070P.
 XX PA (CORI-) CORIXA CORP.
 XX PI Cheever MA, Gaiger A;
 XX WI; 2001-648218/74.
 DR Composition for the treatment of mesothelioma comprises specific peptides i.e. Wilms' tumour antigen polypeptide derived antigenic fragments -
 PS Claim 1; Page 24; 242pp; English.
 XX The invention relates to the use of a composition comprising at least a first isolated peptide, of between 9 and 40 amino acids or a first nucleic acid, encoding the peptide, in the manufacture of a medicament for treating or preventing mesothelioma. The peptides are antigenic peptides derived from the Wilms' tumour protein WT1. The composition is useful for the treatment of mesothelioma, Wilms' tumour, preferably pleural mesothelioma and other WT1 associated malignancies e.g. leukaemia (including acute myeloid leukemia, ALL, chronic myeloid leukemia, CML, acute lymphocytic leukemia, ALL, and childhood ALL), myelodysplastic syndromes, myeloproliferative syndromes and cancers (e.g. breast, testicular, prostate, lung and ovarian) in mammals, preferably humans. The present sequence is an antigenic peptide of the invention derived from mouse WT1.
 CC Sequence 9 AA;
 SO
 Query Match 100.0%; Score 51; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RMPFNAPYL 9
 DB 1 RMPFNAPYL 9
 RESULT 7
 AAG62002 standard; Peptide; 9 AA.
 ID AAG62002 standard; Peptide; 9 AA.
 AC AAG62002;
 XX 06-JUL-2001 (first entry)
 DT Human WT1 immunogenic peptide SEQ ID NO: 185.
 DE Human; mouse; immunotherapy; cancer; leukemia; WT1; Wilms' tumour gene; chromosome 11p13; zinc finger transcription factor.
 KW Homo sapiens.
 OS Homo sapiens.
 XX WO200125273-A2.
 XX PN 12-APR-2001.
 XX PD 04-OCT-2000; 2000WO-US27465.
 XX PF
 XX

PR 04-OCT-1999; 99US-0157459.
 XX (CORI-) CORIXA CORP.
 XX PA Skelky YAW, Xu J, Cheever MA, Reed SG;
 XX WI; 2001-328324/34.
 DR Polypeptide comprising part of the Wilms' Tumour gene product sequence is used in the diagnosis and treatment of malignant diseases e.g. leukemia and cancer associated with WT1 -
 PS Claim 4; Page 183; 228pp; English.
 XX The present invention describes compositions comprising peptides derived from the Wilms' tumour protein WT1 and methods for their use in treating malignant diseases. Peptides derived from both the murine and human WT1 proteins are provided. The human WT1 gene is found on chromosome 11p13, and the protein was shown to be a zinc finger transcription factor. The immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukemia. The present sequence is a polypeptide described in the exemplification of the invention.
 CC Sequence 9 AA;
 SO
 Query Match 100.0%; Score 51; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RMPFNAPYL 9
 DB 1 RMPFNAPYL 9
 RESULT 8
 AAG62110 standard; Peptide; 9 AA.
 ID AAG62110 standard; Peptide; 9 AA.
 AC AAG62110;
 XX 06-JUL-2001 (first entry)
 DT Mouse WT1 immunogenic peptide SEQ ID NO: 293.
 DE Human; mouse; immunotherapy; cancer; leukemia; WT1; Wilms' tumour gene; chromosome 11p13; zinc finger transcription factor.
 KW Mus musculus.
 OS Mus musculus.
 XX WO200125273-A2.
 XX PN 12-APR-2001.
 XX PD 04-OCT-2000; 2000WO-US27465.
 XX PF 04-OCT-1999; 99US-0157459.
 XX PR (CORI-) CORIXA CORP.
 XX PA Skelky YAW, Xu J, Cheever MA, Reed SG;
 XX WI; 2001-328324/34.
 DR Polypeptide comprising part of the Wilms' Tumour gene product sequence is used in the diagnosis and treatment of malignant diseases e.g. leukemia and cancer associated with WT1 -
 PS Claim 4; Page 200; 228pp; English.
 XX The present invention describes compositions comprising peptides derived from the Wilms' tumour protein WT1 and methods for their use in treating malignant diseases. Peptides derived from both the murine and human WT1 proteins are provided. The human WT1 gene is found on chromosome 11p13,
 CC

CC and the protein was shown to be a zinc finger transcription factor. The
 CC immunogenic peptides of the invention are particularly useful in the
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is
 CC a polypeptide described in the exemplification of the invention.

CC Sequence 9 AA;
 SQ

Query Match
 Best Local Similarity 100.0%; Score 51; DB 22; Length 9;
 Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMEPNAPYL 9
 |||||
 1 RMEPNAPYL 9

RESULT 9
 ABG79100
 ID ABG79100 standard; Peptide; 9 AA.
 AC ABG79100;
 XX
 XX 15-NOV-2002 (first entry)

XX Human WT1 class I HLA widely expressed antigen, peptide #1.

XX Cell penetrating peptide; cancer; tumour; melanoma; chlyoma; antigen;
 KW Lymphoma; sarcoma; lung cancer; non-Hodgkin's Lymphoma; Leukaemia;
 KW Hodgkin's Lymphoma; uterine cancer; cervical cancer; bladder cancer;
 KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
 KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
 KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
 KW cytostatic; human.

OS Homo sapiens.
 XX
 XX MO200264057-A2.
 XX
 XX 22-AUG-2002.

XX 15-FEB-2002; 2002WO-US05212.

XX 15-FEB-2001; 2001US-268687P.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Wang R;
 XX
 XX

XX WPI; 2002-627577/67.

XX Novel composition for treating a disease in an animal, comprises an
 PT immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody -
 XX
 XX

XX Disclosure; Page 19; 61pp; English.

XX The invention relates to a composition (I) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (1) a vaccine comprising (I), CPP
 CC associated with an antigen, and a pharmaceutically acceptable carrier
 CC and (2) preparing a composition for a disease, by providing (I)
 CC and CPP associated with an antigen for disease, and introducing the
 CC antigen-associated CPP to (1), where antigen enters into the cell.
 CC The antigens are, for example, tumour antigen derived epitopes
 CC recognised by tumour infiltrating lymphocytes (TIL) of HLA (human
 CC leukocyte antigen) class I or II. The composition is useful for enhancing
 CC immunity in an animal to a disease, by administering a mature dendritic
 CC cell comprising CPP associated with an antigen to disease, to the animal,
 CC such that following the administration, animal is protected from disease,
 CC where the animal comprises both CD4+ and CD8+ T cells. It is also useful
 CC for treating a disease (e.g., cancer, tumour, melanoma, thymoma,
 CC Lymphoma, sarcoma, lung cancer, non-Hodgkin's Lymphoma, Leukaemia,
 CC Hodgkin's Lymphoma, uterine cancer, cervical cancer, bladder cancer,

CC kidney cancer, adenocarcinoma, breast cancer, prostate cancer,
 CC ovarian cancer and pancreatic cancer). The animal is further subjected to
 CC a cancer treatment including surgery, radiation, chemotherapy or gene
 CC therapy. The administration of (I), preferably dendritic cell is prior
 CC to, subsequent to or concurrent with, the cancer treatment. The present
 CC sequence is a tumour antigen derived epitope for inclusion in the
 CC composition of the invention.

XX Sequence 9 AA;
 SQ

Query Match
 Best Local Similarity 100.0%; Score 51; DB 23; Length 9;
 Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMEPNAPYL 9
 |||||
 1 RMEPNAPYL 9

RESULT 10
 ABG33239
 ID ABG33239 standard; Peptide; 9 AA.
 AC ABG33239;
 XX
 XX 15-JUL-2002 (first entry)

XX Human WT1 immunogenic peptide #162.

XX Human; mouse; cytostatic; immunostimulant; WT1; cancer;
 KW immune response.
 KW Homo sapiens.
 OS
 XX
 XX MO200228414-A1.
 XX
 XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US31139.

XX 06-OCT-2000; 2000US-0684361.

XX 09-OCT-2000; 2000US-0685830.

XX 15-FEB-2001; 2001US-0785019.

XX 24-AUG-2001; 2001US-0938864.

XX (CORI-) CORIXA CORP.
 XX (GAIG/) GAIGER A.
 XX
 XX Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
 PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
 PI WPI; 2002-352217/38.

XX Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
 PT treating and diagnosing cancer in a patient -
 XX
 XX

XX Example 4; Page 194; 260pp; English.

XX The invention relates to an isolated WT1 polynucleotide (I) and
 CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
 CC are used for treating and detecting cancer in a patient, and for
 CC stimulating an immune response in patient. ABG33070-ABG33405
 CC represent WT1 amino acid sequences of the invention.

XX Sequence 9 AA;
 SQ

Query Match
 Best Local Similarity 100.0%; Score 51; DB 23; Length 9;
 Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMEPNAPYL 9
 |||||
 1 RMEPNAPYL 9

PW MO200018795-A2.
 XX 06-APR-2000.
 PD 30-SEP-1999; 99WO-US22819.
 XX 30-SEP-1999; 98US-0164223.
 PR 25-MAR-1999; 99US-0276484.
 XX (CORI-) CORIXA CORP.
 PA (GAIIG/) GAIIGER A.
 PI Galger A, Cheever M;
 DR WPI; 2000-293107/25.
 XX
 PR Novel polypeptides comprising an immunogenic portion of a native WTI
 PT polypeptide, useful for inhibiting the development of malignant
 PR diseases associated with WTI expression e.g. leukemia or cancer
 XX
 PS Claim 4; Page 149; 193pp; English.
 XX
 CC The present invention describes polypeptides (I) comprising an
 CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,
 CC WTI. (Or variants of the immunogenic portion retaining the ability to
 CC react with WTI-specific antisera and/or T-cell lines or clones) and
 CC comprising 16 consecutive amino acids (aa) or less of a native WTI
 CC polypeptide. The polypeptides are useful therapeutically and to
 CC manufacture medicaments for enhancing/inducing an immune response in
 CC patients. The polypeptides, mimetics or polynucleotides can be included
 CC with a carrier/excipient in pharmaceutical compositions or with a
 CC non-specific immune response enhancer (e.g. an adjuvant or enhancer
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
 CC compositions and vaccines can be administered to human patients to
 CC enhance or induce an immune response specific for WTI or a cell
 CC expressing WTI, useful to inhibit the development of malignant diseases
 CC associated with WTI expression, e.g. leukemia (especially acute/chronic
 CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).
 CC AAAY98501 to AAAY98811 represent polypeptide sequences, and AAA13848 to
 CC AAA13862 represent PCR primers, used in the exemplification of the
 CC present invention.
 CC
 XX
 SQ Sequence 9 AA;
 Query Match 92.2%; Score 47; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PD 30-AUG-2001.
 XX 22-FEB-2001; 2001WO-US05702.
 PF 22-FEB-2000; 2000US-184070P.
 PR (CORI-) CORIXA CORP.
 PA Cheever MA, Galger A;
 PI WPI; 2001-648218/74.
 DR
 XX
 PR Composition for the treatment of mesothelioma comprises specific
 PT peptides i.e. Wilm's tumour antigen polypeptide derived antigenic
 PR fragments -
 XX
 PS Claim 1; Page 209; 242pp; English.
 XX
 CC The invention relates to the use of a composition comprising at least a
 CC first isolated peptide, of between 9 and 40 amino acids or a first
 CC nucleic acid, encoding the peptide, in the manufacture of a medicament
 CC for treating or preventing mesothelioma. The peptides are antigenic
 CC peptides derived from the Wilm's tumour protein WTI. The composition is
 CC useful for the treatment of mesothelioma, Wilm's tumour, preferably
 CC pleural mesothelioma and other WTI associated malignancies e.g.
 CC leukemia (including acute myeloid leukemia, ALL, chronic myeloid
 CC leukemia, CML, acute lymphocytic leukemia, ALL, and childhood ALL),
 CC myelodysplastic syndromes, myeloproliferative syndromes and cancers
 CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,
 CC preferably humans. The present sequence is an antigenic peptide of
 CC the invention derived from human WTI.
 CC
 XX
 SQ Sequence 9 AA;
 Query Match 92.2%; Score 47; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPY 8
 DB 2 RMPFNAPY 9
 RESULT 14
 AAU68622
 AAU68622 standard; Peptide; 9 AA.
 AC AAU68622;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Human Wilm's tumour protein, WTI, antigenic peptide #17.
 XX
 KW Human; Wilm's tumour; WTI; pleural mesothelioma; antigen;
 KW Leukaemia; acute myeloid leukaemia; ALL; chronic myeloid leukaemia; CML;
 KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;
 KW myeloproliferative syndrome; cancer; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200162920-A2.
 XX

PD 30-AUG-2001.
 XX 22-FEB-2001; 2001WO-US05702.
 PF 22-FEB-2000; 2000US-184070P.
 PR (CORI-) CORIXA CORP.
 PA Cheever MA, Galger A;
 PI WPI; 2001-648218/74.
 DR
 XX
 PR Composition for the treatment of mesothelioma comprises specific
 PT peptides i.e. Wilm's tumour antigen polypeptide derived antigenic
 PR fragments -
 XX
 PS Claim 1; Page 209; 242pp; English.
 XX
 CC The invention relates to the use of a composition comprising at least a
 CC first isolated peptide, of between 9 and 40 amino acids or a first
 CC nucleic acid, encoding the peptide, in the manufacture of a medicament
 CC for treating or preventing mesothelioma. The peptides are antigenic
 CC peptides derived from the Wilm's tumour protein WTI. The composition is
 CC useful for the treatment of mesothelioma, Wilm's tumour, preferably
 CC pleural mesothelioma and other WTI associated malignancies e.g.
 CC leukemia (including acute myeloid leukemia, ALL, chronic myeloid
 CC leukemia, CML, acute lymphocytic leukemia, ALL, and childhood ALL),
 CC myelodysplastic syndromes, myeloproliferative syndromes and cancers
 CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,
 CC preferably humans. The present sequence is an antigenic peptide of
 CC the invention derived from human WTI.
 CC
 XX
 SQ Sequence 9 AA;
 Query Match 92.2%; Score 47; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPY 8
 DB 2 RMPFNAPY 9
 RESULT 15
 AAG61855
 AAG61855 standard; Peptide; 9 AA.
 AC AAG61855;
 XX
 DT 06-JUL-2001 (first entry)
 XX
 DE Human WTI immunogenic peptide SEQ ID NO: 38.
 XX
 KW Human; mouse; immunotherapy; cancer; leukaemia; WTI; Wilm's tumour gene;
 KW chromosome 11p13; zinc finger transcription factor.
 XX
 OS Homo sapiens.
 XX
 PN WO200125273-A2.
 XX
 PD 12-APR-2001.
 XX
 DE 04-OCT-2000; 2000WO-US27465.
 XX
 PR 04-OCT-1999; 99US-0157459.
 XX
 PA (CORI-) CORIXA CORP.
 PI Skelky YAM, Xu J, Cheever MA, Reed SG;
 DR WPI; 2001-328324/34.
 XX
 PR Polypeptide comprising part of the Wilm's Tumour gene product sequence is

PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT and cancer associated with WT1
XX
PS Claim 4; Page 161; 228pp; English.
XX

CC The present invention describes compositions comprising peptides derived
CC from the Wilms' tumor protein WT1 and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WT1
CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukemia. The present sequence is
CC a polypeptide described in the exemplification of the invention.
XX
SQ Sequence 9 AA;

Query Match 97.2%; Score 47; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPY 8
Db 2 RMPFNAPY 9

Search completed: January 21, 2004, 08:51:04
Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 21, 2004, 08:52:21 : Search time 32 Seconds
(without alignments)
57.510 Million cell updates/sec

Title: US-09-625-963A-1

Perfect score: 51

Sequence: 1 RMPFNAPYL 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 762491 seqs, 204481190 residues 81252

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	US-09-872-832-46	Sequence 46, App1
2	51	100.0	9	US-09-938-864-185	Sequence 185, App
3	51	100.0	9	US-09-938-864-293	Sequence 293, App
4	51	100.0	9	US-09-791-477-185	Sequence 185, App
5	51	100.0	9	US-09-791-477-293	Sequence 293, App
6	51	100.0	9	US-09-785-019-185	Sequence 185, App
7	51	100.0	9	US-09-785-019-293	Sequence 293, App
8	51	100.0	9	US-10-210-148-54	Sequence 54, App1
9	51	100.0	9	US-10-195-835-185	Sequence 185, App
10	51	100.0	9	US-10-195-835-293	Sequence 293, App
11	51	100.0	9	US-10-286-333-185	Sequence 185, App
12	51	100.0	9	US-10-286-333-293	Sequence 293, App
13	51	100.0	9	US-10-244-830-185	Sequence 185, App
14	51	100.0	9	US-10-244-830-293	Sequence 293, App
15	51	100.0	9	US-10-125-635A-185	Sequence 185, App

Result No.	Score	Query Match	Length	ID	Description
16	51	100.0	9	US-10-125-635A-293	Sequence 293, App
17	51	100.0	9	US-10-002-603-185	Sequence 185, App
18	51	100.0	9	US-10-002-603-293	Sequence 293, App
19	47	92.2	9	US-09-938-864-38	Sequence 38, App1
20	47	92.2	9	US-09-791-477-38	Sequence 38, App1
21	47	92.2	9	US-09-785-019-38	Sequence 38, App1
22	47	92.2	9	US-10-195-835-38	Sequence 38, App1
23	47	92.2	9	US-10-286-333-38	Sequence 38, App1
24	47	92.2	9	US-10-244-830-38	Sequence 38, App1
25	47	92.2	9	US-10-125-635A-38	Sequence 38, App1
26	47	92.2	9	US-10-002-603-38	Sequence 38, App1
27	46	90.2	9	US-09-938-864-324	Sequence 324, App
28	46	90.2	9	US-09-791-477-324	Sequence 324, App
29	46	90.2	9	US-09-785-019-324	Sequence 324, App
30	46	90.2	9	US-10-195-835-324	Sequence 324, App
31	46	90.2	9	US-10-286-333-324	Sequence 324, App
32	46	90.2	9	US-10-244-830-324	Sequence 324, App
33	46	90.2	9	US-10-125-635A-324	Sequence 324, App
34	46	90.2	9	US-10-002-603-324	Sequence 324, App
35	41	80.4	9	US-09-938-864-79	Sequence 79, App1
36	41	80.4	9	US-09-791-477-79	Sequence 79, App1
37	41	80.4	9	US-09-785-019-79	Sequence 79, App1
38	41	80.4	9	US-10-195-835-79	Sequence 79, App1
39	41	80.4	9	US-10-286-333-79	Sequence 79, App1
40	41	80.4	9	US-10-244-830-79	Sequence 79, App1
41	41	80.4	9	US-10-125-635A-79	Sequence 79, App1
42	41	80.4	9	US-10-002-603-79	Sequence 79, App1
43	41	80.4	9	US-10-286-333-267	Sequence 267, App
44	41	80.4	9	US-10-244-830-267	Sequence 267, App
45	41	80.4	9	US-10-125-635A-267	Sequence 267, App

ALIGNMENTS

RESULT 1
US-09-872-832-46
; Sequence 46, Application US/09872832
; Patent No. US20020131960A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 830002-2003.1
; CURRENT APPLICATION NUMBER: US/09/872,832
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/209,157
; PRIOR FILING DATE: 2000-02-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 46
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-872-832-46

Query Match	Similarity	Score	DB ID	Length
Beat Local	100.0%	51	US-09-938-864-185	9
Matches	9	Conservative	0	Mismatches
			0	Indels
			0	Gaps
			0	Indels
			0	Gaps

RESULT 2
US-09-938-864-185
; Sequence 185, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus

```

; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mosseman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-185

```

```

Query Match      100.0%; Score 51; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

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RESULT 3
US-09-938-864-293
; Sequence 293, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mosseman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-938-864-293

```

```

Query Match      100.0%; Score 51; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

```

```

RESULT 4
US-09-791-477-185
; Sequence 185, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS

```

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; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-185

```

```

Query Match      100.0%; Score 51; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

```

```

RESULT 5
US-09-791-477-293
; Sequence 293, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-477-293

```

```

Query Match      100.0%; Score 51; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

```

```

RESULT 6
US-09-785-019-185
; Sequence 185, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0

```

```

; SEQ ID NO 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-185

```

```

Query Match      100.0%; Score 51; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        1 RMPFNAPYL 9
Db

```

```

RESULT 7
US-09-785-019-293
; Sequence 293, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-785-019-293

```

```

Query Match      100.0%; Score 51; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        1 RMPFNAPYL 9
Db

```

```

RESULT 8
US-10-210-148-54
; Sequence 54, Application US/10210148
; Publication No. US20030171280A1
; GENERAL INFORMATION:
; APPLICANT: Soderstrom, Karl Peter
; TITLE OF INVENTION: Compositions And Methods For Modulation Of Immune Response
; FILE REFERENCE: TR0M0002
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: PCT/US02/24311
; PRIORITY FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatencIn version 3.2
; SEQ ID NO 54
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-148-54

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```

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        1 RMPFNAPYL 9
Db

```

```

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        1 RMPFNAPYL 9
Db

```

```

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        1 RMPFNAPYL 9
Db

```

```

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        1 RMPFNAPYL 9
Db

```

```

Oy      1 RMPFNAPYL 9
        |||||
        1 RMPFNAPYL 9
Db

```

```

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        1 RMPFNAPYL 9
Db

```

```

RESULT 9
US-10-195-835-185
; Sequence 185, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Mossman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C8
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-195-835-185

```

```

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        1 RMPFNAPYL 9
Db

```

```

RESULT 10
US-10-195-835-293
; Sequence 293, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Mossman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C8
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-195-835-293

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```

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        1 RMPFNAPYL 9
Db

```

```

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        1 RMPFNAPYL 9
Db

```

```

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        1 RMPFNAPYL 9
Db

```

```

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 RMPFNAPYL 9
        |||||
        1 RMPFNAPYL 9
Db

```

Db 1 RMPFNAPYL 9

RESULT 11
US-10-286-333-185
; Sequence 185, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Java, No. US20030215458A1a1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-286-333-185

Query Match 100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

RESULT 12
US-10-286-333-293
; Sequence 293, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Java, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-286-333-293

Query Match 100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

RESULT 13
US-10-244-830-185
; Sequence 185, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-244-830-185

Query Match 100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FILE REFERENCE: 210121.465C9
CURRENT APPLICATION NUMBER: US/10/244,830
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 468
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 185
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapien
US-10-244-830-185

Query Match 100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

RESULT 14
US-10-244-830-293
; Sequence 293, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Java, No. US20030235557A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-244-830-293

Query Match 100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9
Db 1 RMPFNAPYL 9

RESULT 15
US-10-125-635A-185
; Sequence 185, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Carter, Darrick D.
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-125-635A-185

Query Match 100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPNAPYL 9
| | | | | | | | | |
Db 1 RMPNAPYL 9

Search completed: January 21, 2004, 08:57:41
Job time : 32 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 21, 2004, 08:50:15 ; Search time 22 Seconds
(without alignments)
17.309 Million cell updates/sec

Title: US-09-625-963A-1

Perfect score: 51

Sequence: 1 RMPNAPYL 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310958 residues

Total number of hits satisfying chosen parameters: 77717

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA:*

2: /cgn2_6/ptodata/1/aa/5A.COMB.pep:*

3: /cgn2_6/ptodata/1/aa/6A.COMB.pep:*

4: /cgn2_6/ptodata/1/aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/1/aa/PCTUS.COMB.pep:*

6: /cgn2_6/ptodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	56.9	9	4	US-09-493-543-158
2	28	54.9	9	3	US-09-163-368B-26
3	28	54.9	9	3	US-09-161-877B-26
4	27	52.9	8	2	US-08-737-085A-6
5	27	52.9	8	3	US-09-246-258-6
6	27	52.9	8	3	US-09-532-106-6
7	27	52.9	8	4	US-09-839-666-6
8	26	51.0	6	2	US-08-672-805-12
9	26	51.0	8	3	US-08-540-922D-8
10	25	49.0	8	3	PCT-US94-03744-6
11	25	49.0	9	3	US-09-162-368B-28
12	25	49.0	7	1	US-09-161-877B-28
13	25	49.0	7	1	US-08-261-525A-6
14	24	47.1	7	4	US-09-367-940A-1
15	24	47.1	9	2	US-08-417-174-13
16	24	47.1	9	2	US-08-231-565A-13
17	24	47.1	9	2	US-09-007-961-13
18	24	47.1	9	3	US-08-159-339A-93
19	24	47.1	9	3	US-09-163-368B-24
20	24	47.1	9	3	US-09-161-877B-24
21	24	47.1	9	3	US-08-786-455B-5
22	24	47.1	9	3	US-09-267-439-13
23	24	47.1	9	4	US-09-311-784A-198
24	24	47.1	7	4	US-09-073-138-13
25	23	45.1	8	6	5514590-12
26	23	45.1	8	2	US-08-177-109A-24
27	23	45.1	8	2	US-08-687-706-24

28	23	45.1	8	3	US-08-444-818-433	Sequence 433, App
29	23	45.1	8	3	US-08-444-818-434	Sequence 434, App
30	23	45.1	8	5	PCT-US94-01321-70	Sequence 70, App
31	22	43.1	6	2	US-08-672-805-111	Sequence 11, App
32	22	43.1	7	4	US-09-461-325-321	Sequence 321, App
33	22	43.1	8	3	US-09-484-319-7	Sequence 7, App
34	22	43.1	8	3	US-09-484-319-7	Sequence 7, App
35	22	43.1	8	3	US-09-484-320-7	Sequence 7, App
36	22	43.1	8	3	US-09-484-321-7	Sequence 7, App
37	22	43.1	8	3	US-09-484-323-7	Sequence 7, App
38	22	43.1	8	3	US-09-325-769-8	Sequence 8, App
39	22	43.1	8	3	US-09-636-170-7	Sequence 7, App
40	22	43.1	8	3	US-09-637-518-7	Sequence 7, App
41	22	43.1	8	4	US-09-757-933B-8	Sequence 8, App
42	22	43.1	9	3	US-09-152-368B-25	Sequence 25, App
43	22	43.1	9	3	US-09-161-877B-25	Sequence 25, App
44	22	43.1	9	4	US-09-492-543-180	Sequence 180, App
45	22	43.1	9	4	US-09-461-325-386	Sequence 386, App

ALIGNMENTS

RESULT 1
US-09-492-543-158
Sequence 158, Application US/09492543A
Patent No. 6316213
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: D6223CIP-B
CURRENT APPLICATION NUMBER: US/09/492,543A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 189
SOFTWARE: WORD 6.0.1 for Macintosh
SEQ ID NO 158
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: Residues 96-104 of the PUMP-1 protein

Query Match 56.9%; Score 29; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 2 MFPNAP 7
2 LFPNAP 7

RESULT 2
US-09-162-368B-26
Sequence 26, Application US/09162368B
Patent No. 6083703
GENERAL INFORMATION:
APPLICANT: WANG, R. F.; ROSENBERG, S. A.
TITLE OF INVENTION: IDENTIFICATION OF TRP-2 AS
TITLE OF INVENTION: A HUMAN TUMOR ANTIGEN RECOGNIZED BY CYTOTOXIC T
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:

```

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,368B
FILING DATE: 28-SEPT-1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,736
FILING DATE: 04-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,602
FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34,556
REFERENCE/DOCKET NUMBER: 2026-4243US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-162-368B-26

```

```

Query Match 54.9%; Score 28; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.5e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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```

QY 2 MFPNAPY 8
DB 2 LFPGRPY 8

```

```

RESULT 3
US-09-161-877B-26
Sequence 26, Application US/09161877B
Patent No. 6132980
GENERAL INFORMATION:
APPLICANT: WANG, R.F.; ROSENBERG, S. A.
TITLE OF INVENTION: IDENTIFICATION OF TRP-2
TITLE OF INVENTION: AS A HUMAN TUMOR ANTIGEN RECOGNIZED BY
TITLE OF INVENTION: CYTOTOXIC T LYMPHOCYTES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/161,877B
FILING DATE: 28-SEPT-1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

```

```

APPLICATION NUMBER: 08/725,736
FILING DATE: 04-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,602
FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34,556
REFERENCE/DOCKET NUMBER: 2026-4243US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-161-877B-26

```

```

APPLICATION NUMBER: 08/725,736
FILING DATE: 04-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,602
FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34,556
REFERENCE/DOCKET NUMBER: 2026-4243US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-161-877B-26

```

```

Query Match 54.9%; Score 28; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.5e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2 MFPNAPY 8
DB 2 LFPGRPY 8

```

```

RESULT 4
US-08-737-085A-6
Sequence 6, Application US/08737085A
Patent No. 5869232
GENERAL INFORMATION:
APPLICANT: SALIBERG, MATTI
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
TITLE OF INVENTION: EXCHANGER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: DARBY & DARBY PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,085A
FILING DATE: 27-DEC-1996
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/OC569
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
TELEFAX: 212-753-6237
TELEX: 236687

```

```

APPLICATION NUMBER: 08/725,736
FILING DATE: 04-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,602
FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34,556
REFERENCE/DOCKET NUMBER: 2026-4243US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-161-877B-26

```

```

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-085A-6

```

```

Query Match 52.9%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Qy 4 PNPATL 9
Db 2 PNPATL 7

```

RESULT 5

```

US-09-246-258-6
; Sequence 6, Application US/09246258
; Patent No. 6040137

```

```

GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: DARBY & DARBY PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/246.258
FILING DATE:
CLASSIFICATION:

```

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/737,085
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
TELEFAX: 212-753-6237
TELEX: 236687

```

```

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-246-258-6

```

```

Query Match 52.9%; Score 27; DB 3; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 4 PNPATL 9
Db 2 PNPATL 7

```

RESULT 6

US-09-532-106-6

```

; Sequence 6, Application US/09532106
; Patent No. 6245895

```

```

GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: DARBY & DARBY PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/532,106
FILING DATE: 21-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/737,085A
FILING DATE: 27-DEC-1996

```

```

ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
TELEFAX: 212-753-6237
TELEX: 236687

```

```

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-532-106-6

```

```

Query Match 52.9%; Score 27; DB 3; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 4 PNPATL 9
Db 2 PNPATL 7

```

RESULT 7

```

US-09-839-666-6
; Sequence 6, Application US/09839666
; Patent No. 6469143

```

```

GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: DARBY & DARBY PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

```

```

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/839,666
FILING DATE: 19-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/737,085
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-839-666-6

Query Match          52.9%; Score 27; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PNAFYL 9
DB 2 PNAFYL 7

RESULT 8
US-08-672-805-12
Sequence 12, Application US/08672805
Patent No. 5831003
GENERAL INFORMATION:
APPLICANT: Baumback, George A.,
APPLICANT: Bueltner, Joseph A.,
APPLICANT: Dadd, Christopher A.,
APPLICANT: Hammond, David J.,
TITLE OF INVENTION: Peptides which bind to Prothrombin and
TITLE OF INVENTION: Thrombin
NUMBER OF INVENTION: 21
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 800 Dwight Way
STREET: P. O. Box 1986
CITY: Berkeley
STATE: California
COUNTRY: USA
ZIP: 94701-1986
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB Storage
COMPUTER: IBM
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,805
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Giblin, James A.
REGISTRATION NUMBER: 25772
REFERENCE/DOCKET NUMBER: MSB-7236
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 705-7910

```

```

TELEFAX: (510) 705-7904
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
STRANDEDNESS: single strand
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: peptide
US-08-672-805-12

Query Match          51.0%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PNAFYL 9
DB 1 PFAFYL 6

RESULT 9
US-08-540-922D-8
Sequence 8, Application US/08540922D
Patent No. 6284476
GENERAL INFORMATION:
APPLICANT: Boon-Fallieur, Thierry; Brichard, Vincent; Van
APPLICANT: Bel, Aline; De Plaen, Etienne; Pierre,
APPLICANT: Renaud Jean-Christophe; Wollet, Thomas; and
APPLICANT: Lethe, Bernard.
TITLE OF INVENTION: METHOD OF IDENTIFYING INDIVIDUALS SUFFERING
TITLE OF INVENTION: FROM A CELLULAR ABNORMALITY SOME OF WHOSE
TITLE OF INVENTION: ABNORMAL CELLS PRESENT COMPLEXES OF HUMAN
TITLE OF INVENTION: LEUCOCYTE ANTIGEN TYROSINASE DERIVED
TITLE OF INVENTION: PEPTIDES, AND METHODS FOR TREATING SAID
TITLE OF INVENTION: INDIVIDUALS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,922D
FILING DATE: October 11, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,714
FILING DATE: 28 April 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/994,928
FILING DATE: 22 December 1992
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5299.5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: Protein

```

```

FEATURE:
OTHER INFORMATION: SEQ of aa corresponding to nt 1816-1839
OTHER INFORMATION: nt of SEQ ID NO: 1
US-08-540-922D-8

```

```

Query Match          51.0%; Score 26; DB 3; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.5e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy 3 PNNAPYL 9
    |||
    2 FPLSPYV 8
Db

```

```

RESULT 10
PCT-US94-03744-6
Sequence 6, Application PC/TUS9403744
GENERAL INFORMATION:
APPLICANT: PETRI, WILLIAM A.
APPLICANT: MCCOY, JAMES J.
APPLICANT: MANN, BARBARA J.
TITLE OF INVENTION: 35/31 KDA SUBUNIT OF THE
TITLE OF INVENTION: ENTAMOEBA
TITLE OF INVENTION: HISTOXYTICA ADHERENCE LECTIN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Morrison & Feerster
STREET: 2000 Pennsylvania Avenue, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03744
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,679
FILING DATE: 09-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29148-20005.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-03744-6

```

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Query Match          49.0%; Score 25; DB 5; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 4 PNNAPY 8
    |||
    3 PNYPY 7
Db

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RESULT 11
US-09-162-368B-28
Sequence 28, Application US/09162368B
Patent No. 6083703

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GENERAL INFORMATION:
APPLICANT: WANG, R. F.; ROSENBERG, S. A.
TITLE OF INVENTION: IDENTIFICATION OF TRP-2 AS
TITLE OF INVENTION: A HUMAN TUMOR ANTIGEN RECOGNIZED BY CYTOTOXIC T
TITLE OF INVENTION: LYMPHOCYTES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,368B
FILING DATE: 28-SEPT-1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,736
FILING DATE: 04-OCT-1996
APPLICATION NUMBER: 08/599,602
FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34,556
REFERENCE/DOCKET NUMBER: 2026-4243US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-162-368B-28

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Query Match          49.0%; Score 25; DB 3; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Oy 4 PNNAPY 8
    |||
    4 PGAPY 8
Db

```

```

RESULT 12
US-09-161-877B-28
Sequence 28, Application US/09161877B
Patent No. 6132980
GENERAL INFORMATION:
APPLICANT: WANG, R. F.; ROSENBERG, S. A.
TITLE OF INVENTION: IDENTIFICATION OF TRP-2
TITLE OF INVENTION: AS A HUMAN TUMOR ANTIGEN RECOGNIZED BY
TITLE OF INVENTION: CYTOTOXIC T LYMPHOCYTES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE

```

```

? CITY: NEW YORK
? STATE: NEW YORK
? COUNTRY: USA
? ZIP: 10154
? COMPUTER READABLE FORM:
? MEDIUM TYPE: FLOPPY DISK
? OPERATING SYSTEM: IBM PC COMPATIBLE
? SOFTWARE: MICROSOFT WORD 97
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/161,877B
? FILING DATE: 28-SEPT-1998
? CLASSIFICATION: 530
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/725,736
? FILING DATE: 04-OCT-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/599,602
? FILING DATE: 09-FEB-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: KATHRYN M. BROWN
? REGISTRATION NUMBER: 34,556
? REFERENCE/DOCKET NUMBER: 2026-4243US2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 758-4800
? TELEFAX: (212) 751-6849
? TELEX: 421792
? INFORMATION FOR SEQ ID NO: 28:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 9
? TYPE: AMINO ACID
? STRANDEDNESS: UNKNOWN
? TOPOLOGY: UNKNOWN
? MOLECULE TYPE:
? DESCRIPTION: PEPTIDE
? FEATURE:
? NAME/KEY:
? LOCATION:
? IDENTIFICATION METHOD:
? OTHER INFORMATION:
?
? US-09-161-877B-28

```

```

Query Match 49.0%; Score 25; DB 3; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 PNPAP 8
Db 4 PGAPY 8

```

```

RESULT 13
US-08-261-525A-6
; Sequence 6, Application US/08261525A
; Patent No. 5569598
; GENERAL INFORMATION:
; APPLICANT: PARK, Soon Jae
; APPLICANT: LEE, Young Mee
; APPLICANT: WON, Teug Yeon
; APPLICANT: KWON, Soon Chang
; APPLICANT: LEE, Seung Joo
; APPLICANT: KIM, Jung Ho
; APPLICANT: KIM, Bum Joon
; TITLE OF INVENTION: NOVEL AMINOPEPTIDASE, PROCESSES FOR
; TITLE OF INVENTION: THE PREPARATION OF AMINOPEPTIDASE AND
; TITLE OF INVENTION: PROTEIN THEREFROM
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARK, Soon Jae
; STREET: Lucky Apt. 6-101, Doryong-dong, Yuseong-gu
; CITY: Daejeon
; STATE: Daejeon
; COUNTRY: Republic of Korea

```

```

? ZIP: 305-340
? ADDRESSER: LEE, Young Mee
? STREET: Shinsung Apt. 3-306, 28-4, Nae-dong, Seo-gu
? CITY: Daejeon
? STATE: Daejeon
? COUNTRY: Republic of Korea
? ZIP: 302-181
? ADDRESSER: WON, Teug Yeon
? STREET: Gongjak Hanyang Apt. 3-1201, 835,
? STREET: Tandang-dong, Seo-gu
? CITY: Daejeon
? STATE: Daejeon
? COUNTRY: Republic of Korea
? ZIP: 302-223
? ADDRESSER: KWON, Soon Chang
? STREET: Shinsung Apt. 3-107, 28-4, Nae-dong, Seo-gu
? CITY: Daejeon
? STATE: Daejeon
? COUNTRY: Republic of Korea
? ZIP: 302-181
? ADDRESSER: LEE, Seung Joo
? STREET: Lucky Apt. B-107, 386-4, Doryong-dong,
? STREET: Yuseong-gu
? CITY: Daejeon
? STATE: Daejeon
? COUNTRY: Republic of Korea
? ZIP: 305-340
? ADDRESSER: KIM, Jung Ho
? STREET: Lucky Dormitory 511, 386-1, Doryong-dong,
? STREET: Yuseong-gu
? CITY: Daejeon
? STATE: Daejeon
? COUNTRY: Republic of Korea
? ZIP: 305-340
? ADDRESSER: KIM, Bum Joon
? STREET: Lucky Dormitory 502, 386-1, Doryong-dong,
? STREET: Yuseong-gu
? CITY: Daejeon
? STATE: Daejeon
? COUNTRY: Republic of Korea
? ZIP: 305-340
? ADDRESSER: LEE, Seung Joo
? STREET: Lucky Apt. B-107, 386-4, Doryong-dong,
? STREET: Yuseong-gu
? CITY: Daejeon
? STATE: Daejeon
? COUNTRY: Republic of Korea

```

```

Query Match 47.1%; Score 24; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 MFPNAP 7

```

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US-08-261-525A-6
; MOLECULE TYPE: peptide
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk, 3.5 inch, 1.44MB storage
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,525A
; FILING DATE: 17-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 93-11107
; FILING DATE: 17-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Shahan Islam
; REGISTRATION NUMBER: 32,507
; REFERENCE/DOCKET NUMBER: A-9883
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-1000
; TELEFAX: (212) 953-7249
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-261-525A-6

```

Db 1 MFPTP 6

RESULT 14
US-09-367-940A-1
; Sequence 1, Application US/09367940A
; Patent No. 6428997

GENERAL INFORMATION:

APPLICANT: LG CHEMICAL LTD.
LEE, Young-Phil
HAN, Kyuboem
KIM, Se-Hoon
PARK, Soon-Jae
LEE, Seung-Joo

TITLE OF INVENTION: Aminopeptidase
derived from Bacillus licheniformis
and process for preparation of natural
type proteins

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSER: BACHMAN & LAPOINTE, P.C.
STREET: Suite 1201, 900 Chapel Street
CITY: New Haven
STATE: Connecticut
COUNTRY: U.S.A.
ZIP: 06510-2802

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage

COMPUTER: IBM

OPERATING SYSTEM: WINDOWS 95/98

SOFTWARE: MS WORD

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/367,940A

FILING DATE: 18-Aug-1999

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1

US-09-367-940A-1

Query Match 47.1%; Score 24; DB 4; Length 7;

Best Local Similarity 66.7%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 MFPTP 7

Db 1 MFPTP 6

RESULT 15

US-08-417-174-13

; Sequence 13, Application US/08417174

; Patent No. 5844075

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

APPLICANT: STEVEN A. MELANOMA ANTIGENS AND

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESSES:

ADDRESSER: MORGAN & PINNIEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-08-417-174-13

Query Match 47.1%; Score 24; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PNP 7

Db 4 PNP 7

Search completed: January 21, 2004, 08:53:24
Job time : 23 secs

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